Programa de Doctorado "Matemáticas"

PhD Dissertation

Sistemas dinámicos en modelos estocásticos con ruido fraccionario

Dynamical systems in stochastic models with fractional noise

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A mis padres y a mi hermana

A Tomás y a María José

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Javier López de la Cruz

Resumen

La presente tesis doctoral, que se enmarca en las ramas de conocimiento del *Análisis Matemático* así como de la *Matemática Aplicada*, está dedicada al modelado y análisis de los efectos causados por diferentes tipos de perturbaciones, tanto estocásticas como aleatorias, en modelos de quimiostato, experimentos de laboratorio realmente interesantes y útiles a la hora de entender numerosos procesos biológicos. Gracias a considerar procesos estocásticos, es posible obtener modelos matemáticos mucho más realistas, desde el punto de vista biológico, que reflejan de una manera más fiel los experimentos que se llevan a cabo en el laboratorio. Las técnicas basadas en la moderna teoría de los Sistemas Dinámicos Aleatorios así como los atractores *pullback* nos permitirán investigar el comportamiento asintótico en tiempo de los correspondientes sistemas estocásticos y, por tanto, podremos obtener información detallada sobre su comportamiento a largo plazo. De esta forma, podremos tomar una decisión acerca de qué tipo de ruido es más adecuado a la hora de modelar diversas situaciones reales.

En el Capítulo 1, nuestro objetivo es analizar los efectos de perturbaciones estocásticas en el flujo de entrada de los modelos de quimiostato haciendo uso del proceso de Wiener estándar. Demostraremos algunos teoremas sobre la existencia y unicidad de solución global así como la existencia y unicidad de un atractor *pullback* aleatorio. Además, mostraremos diversas simulaciones numéricas que reflejarán los resultados teóricos probados a lo largo del capítulo. Sin embargo, podremos observar algunos inconvenientes debidos al uso de este ruido no acotado, por ejemplo, veremos que algunas variables pueden llegar a tomar valores negativos, algo completamente irrealista, aunque el análisis matemático se pueda llevar a cabo sin ningún problema. Otro de los inconvenientes encontrados es que no es posible demostrar la persistence de las especies debido a que el flujo de entrada del quimiostato podría tomar valores arbitrariamente grandes. En vista de los inconvenientes citados, tendremos que tomar una decisión para cambiar la forma de modelar el flujo de entrada del quimiostato ya que, o bien este tipo de ruido no es realista, o bien deberíamos introducirlo de alguna otra forma.

En el Capítulo 2, analizamos los efectos de perturbaciones aleatorias en el flujo de entrada del quimiostato por medio de un proceso de Ornstein-Uhlenbeck. Tal proceso contará con un parámetro de control que nos permitirá controlar el ruido de tal forma que todas sus realizaciones permanezcan en una banda estrictamente positiva para cualquier tiempo. Gracias a esta nueva idea, mucho más realista desde

el punto de vista biológico, también seremos capaces de garantizar la persistencia de las especies en ambos casos, con y sin pared, principal objetivo desde el punto de vista biológico. Demostraremos la existencia y unicidad de solución global y también probaremos la existencia de conjuntos compactos absorbentes y atrayentes para las soluciones de los correspondientes sistemas. No obstante, el aspecto más interesante de este nuevo marco de trabajo es que tales conjuntos no dependerán del ruido y, además, se demostrarán en sentido *forward*, lo cual supone una diferencia significativa con respecto al resto de capítulos de esta tesis doctoral y, también, respecto a los resultados que podemos encontrar en la literatura. Finalmente, mostraremos diversas simulaciones numéricas que reflejarán los resultados demostrados a lo largo del capítulo y haremos una comparación de esta forma de modelar perturbaciones en el flujo de entrada del quimiostato con la que se usa en el Capítulo 1. Gracias a ello, podremos observar las grandes ventajas que tiene el uso del proceso de Ornstein-Uhlenbeck a la hora de modelar este tipo de situaciones. De hecho, en vista de los beneficios tan interesantes que se han logrado a lo largo del desarrollo de esta nueva idea, nos replantearemos visitar otros modelos, no necesariamente sólo los de quimiostato, ya que podrían obtenerse resultados interesantes.

En el Capítulo 3, analizamos los efectos medioambientales causados en los modelos de quimiostato por el proceso de Wiener estándar. Sin embargo, en este caso introduciremos las perturbaciones estocásticas de tal forma que todas las realizaciones del ruido mantengan las soluciones del sistema positivas, hecho razonable desde el punto de vista biológico. En esta ocasión, también conseguiremos ciertas mejoras respecto a los modelos analizados previamente por otros autores, no sólo en el caso estocástico sino también en el determinista. Demostraremos algunos teoremas sobre la existencia y unicidad de solución global, así como la existencia y unicidad de un atractor *pullback* aleatorio. Finalmente, mostraremos algunas simulaciones numéricas que reflejarán los resultados probados a lo largo del capítulo.

Por último, en el Capítulo 4, analizaremos los efectos causados en los modelos de quimiostato por un nuevo proceso estocástico: el movimiento Browniano fraccionario, que es una generalización del proceso de Wiener o movimiento Browniano estándar. Gracias a esta nueva idea, seremos capaces de considerar diferentes tipos de términos de difusión estoćastica que podrán ir mucho más allá de los términos aditivos o lineales multiplicativos, como ocurre el caso caso en el que usamos el proceso de Wiener estándar. Sin embargo, para poder tratar con este nuevo ruido, necesitaremos definir una nueva integral respecto del movimiento Browniano fraccionario, que llamaremos *integral fraccionaria*. Demostraremos la existencia y unicidad de solución global en ciertos espacios de Hölder, sin embargo, en este caso necesitaremos tratar explícitamente con el ruido con lo que necesitaremos introducir una sucesión de tiempos de parada que nos ayude a controlar el tamaño del ruido. De esta forma, probaremos también la existencia y unicidad de un atractor *pullback* aleatorio discreto y, posteriormente, estableceremos la existencia y unicidad del correspondiente atractor *pullback* aleatorio continuo. Posteriormente, realizaremos un análisis de los tiempos de parada que nos permitirá dar sentido a las condiciones impuestas a lo largo del estudio matemático previo, así como realizar algunas conclusiones. Finalmente, mostraremos algunas simulaciones numéricas que nos permitirán observar los efectos de este nuevo ruido con los modelos de quimiostato.

Abstract

This dissertation, which belongs to the field of *Mathematical Analysis* and *Applied Mathematics*, is dedicated to model and analyze the effects caused by different types of stochastic and random perturbations on chemostat models, a laboratory device which is interesting and useful when understanding several biological process. Thanks to considering stochastic processes to perturb the well-known deterministic models, it is possible to obtain mathematical models which are more realistic from the biological point of view and, moreover, fit better the real chemostats displayed in laboratories. In addition, the techniques based on the modern theory of Random Dynamical Systems as well as pullback attractors will allow us to investigate the long-time behavior of the corresponding stochastic systems and, therefore, very detailed information about the asymptotic behavior of our model will be obtained. In such a way, a decision can be made concerning which type of noise is more accurate to handle the situation to be modeled.

In Chapter 1 our aim is to analyze the effects of stochastic disturbances on the input flow in chemostat models by means of the standard Wiener process. We provide some theorems concerning the existence and uniqueness of global solution as well as the existence and uniqueness of a random pullback attractor. In addition, several numerical simulations will be shown to support the results proved through the chapter. Nevertheless, from the previous study, some drawbacks can be found when using this unbounded noise since, for instance, some state variables can take negative values, which is totally unrealistic from the biological point of view even though our mathematical analysis is accurate to handle the mathematical problem. On the other hand, it is not possible to prove the persistence of the species since the disturbed input flow could take values arbitrary large. As a consequence, these inconveniences suggest us that either the fact of perturbing the input flow with such a noise may not be a realistic situation or that we should to use another different approach when modeling disturbances on the input flow of the chemostat device.

In Chapter 2 we analyze the effects of random disturbances on the input flow in chemostat models but, in this case, we use a suitable Ornstein-Uhlenbeck process, involving a control parameter, which will allows us to control the noise such that every realization will remain in a strictly positive interval for every time. Thanks to this new idea, which is more realistic from the biological point of view, we can guarantee the persistence of the species in both chemostat models with and without wall growth which is, needless to say, the main goal pursued by biologists. Some theorems concerning the existence and uniqueness of

global solution as well as the existence of compact absorbing and attracting sets for the solution of our systems are also provided. The most interesting point of this new approach it that the corresponding sets are deterministic and they are provided forwards in time, which is a significant difference with respect to the rest of the chapters on this dissertation and, of course, the results that can be found in the literature as well. Finally, several numerical simulations are shown to support the results in the chapter and compare this way of modeling disturbances on the input flow with the one used in the first chapter. In view of the previous reasons, we will notice the big advantages of making use of the corresponding suitable Ornstein-Uhlenbeck process when modeling this kind of situations. In fact, in view of the interesting benefits coming from this new approach, we will consider to revisit other models, not necessarily only the chemostat ones, since interesting results are expected to be obtained.

In Chapter 3, we analyze the environmental effects in chemostat models by means of the standard Wiener process. Nevertheless, differently to the analysis developed in Chapter 1, in this case we introduce stochastic disturbances in a different way, which will be properly motivated in the corresponding chapter, such that every realization of the noise keep every solution of the model in the first quadrant, which is expected from the biological point of view. In this case, we will achieve also some improvements with respect to chemostat models analyzed previously by other authors in a similar way and also with respect to the results already known about the deterministic ones. Some theorems concerning the existence and uniqueness of global solution as well as the existence and uniqueness of a random pullback attractor will be provided. Finally, some numerical simulations will be also shown to support the results through the chapter.

Eventually, in Chapter 4, we analyze the effects caused on the chemostat model by a new stochastic process: the fractional Brownian motion, which is a generalization of the standard Brownian motion. Thanks to this new approach, we would be able to consider different and more general stochastic diffusion terms, not only additive or linear multiplicative ones as made when considering the standard Wiener process. Nevertheless, in order to deal with this new noise, we will need to define a new integral, called *the fractional integral*, respect to the fractional Brownian motion. A theorem concerning the existence and uniqueness of global solution in some damped Hölder space will be provided. However, we will need to deal with the noise explicitly such that a sequence of stopping times, which will help us to control the size of the noise, will be defined. In such a way, we will prove the existence and uniqueness of a discrete pullback random attractor and, therefore, we will prove the existence and uniqueness of the corresponding continuous one. Therefore, an analysis about the stopping times will be carried out in order to give sense to the conditions assumed along the previous mathematical analysis. Finally, some numerical simulations will be also shown to observe the effects of this new noise on the chemostat models.

Contents

Introduction

In this introductory chapter we will present the chemostat device, which will be the object of study along this dissertation. Some interesting historical details will be provided and the main biological aspects to be taken into account will be carefully explained as well. After that, we will introduce the mathematical equations describing the dynamics of the chemostat and will present some interesting ways to consider either stochasticity or randomness which will allow us to set up much more realistic models than the deterministic ones. In addition, each way will be studied in detail later in the corresponding chapter, so that a decision can be made concerning the way which leads into more realistic models which fit better the real ones.

An excellent introduction about the chemostat device, not only concerning the biological aspects but also the main mathematical ingredients necessary when beginning the study of the corresponding differential systems, can be found in the book [49]. Due to this fact, our introductory chapter is based on the one provided there, in fact, some paragraphs from [49] will be also mentioned in italics whenever it is necessary in order to make our presentation as much nice as possible.

Historical outline

The chemostat is an experimental device invented in the 1950s by Monod (see [66]), and Novick and Szilard (see [67]) at the same time. On the one hand, Monod presented the equations of the chemostat as well as an experimental example in his first paper, whose aim was to control the microbial growth by interacting with the input flow. In addition, Monod proposed the name *bactogène* to refer the chemostat. On the other hand, Novick and Szilard presented a simpler experimental device and they found some technical difficulties when designing a system capable of supplying material to small volume reactor. Moreover, they proposed the name *chemostat* which comes from *chemical* and *static*. In Figure 0.1 (from Google) we can see a photo of Jacques Monod, Aaron Novick and Leo Szilard, respectively from left to right.

Figure 0.1: Jacques Monod, Aaron Novick and Leo Szilard

Concerning the history of the chemostat, it was firstly used by microbiologists in order to study the growth of some species of microorganisms but its usage greatly diversified with the passage of time, in fact, such was the case that it became a prominent tool in microbiology laboratories in the 1960s, shortly after its invention, to study relationships between growth and environment parameters as well as characterizing all kinds of microbes. Nevertheless, the model as a mathematical object was seen as a formal entity. After that, in the 1970s and 1980s, the chemostat became the focus of very interest in mathematical ecology in spite of the fact that it was slightly neglected by microbiologists since they were more interested in the development of molecular biology approaches for the monitoring and understanding of microbial ecosystems. In fact, it was in the 1980s when it enjoyed its moment of glory with Hansen and Hubell's works on competitive exclusion, see [47]. Later, studies on the competition of microorganisms rekindled interest among researchers, specially in the field of microbial ecology. Then, in the 2000s, when it took place the advent of the postgenomic era which required knowledge and fine control of reaction media, a renewed interest in the chemostat device was observed among microbiologists. It was due to the fact that the model satisfies a number of formalization requirements expressed in the field of microbial ecology (see [52]), to such an extent that microbial ecosystems have today become models for general ecology (see [54]). Finally, nowadays, the chemostat is very well understood by engineers and laboratory technicians, in such a way that it is currently used in scientific areas related to the acquisition of knowledge which is essential for ecol-

ogy or evolutionary biology and for applying the model for water treatment, biomass energy recovery and biotechnologies, to name a few of the most interesting applications.

At the present moment, the world of microbial ecology is going through a real revolution due to advances in molecular biology. That is how, from the research for the comprehension of evolution and cellular regulation mechanisms, a new disciplinary field called systems biology has recently emerged. This branch of science, basically multidisciplinary, seeks to understand the cellular mechanisms at the basis of the functioning of living cells. Its objective is clearly visible: to be able in the coming years to propose an "in silico" cell mimicking in every aspect the functioning of a living cell. This would be achieved by simulating its growth from reading its DNA until its division into two daughter cells. One of the difficulties that confronts researchers is to be able to study these cells within stationary environments, which a chemostat precisely allows. Then, new experimental devices have emerged, based on the principle of the chemostat, homogeneous and operating continuously. They are supposed to be able to provide researchers with the set of data that includes the necessary information for the understanding of studied phenomena. In addition, it is rather their utilization in the context of systems biology and, as a result, the renewed interest in the chemostat that is interesting to point out here, see [52, 81].

In the end, it is worth mentioning that the chemostat is not only subject of a large number of publications but also several books which are essential in the fields of mathematics, in fact, many different works can be done concerning such as, in principle, simple device since it can be considered as a main source of uncertainty when biological processes are modeled which lies in modeling the growth rate of microorganisms. In addition, it is also the subject of many studies as a mathematical object. Such was the case that it constitutes a very active branch of applied mathematics. Furthermore, it proposes a formal framework called *theory of the chemostat* centered around a small well-identified community of mathematicians. Concerning its reputation, it is due to the fact that it is capable of fixing the growth rate of the microorganisms that are contained at equilibrium by means of manipulating the input flow, what is more, *the publications in the literature show that the model reproduces the experimental reality particularly accurately by considering all or part of the present ecosystem as functional populations (see [40, 41]), therefore it appeared legitimate to make use of it as a building block, so to speak, in order to move beyond the pure simulation approach and make it possible to address the study of models of complex biological processes in a systematic and generic manner and also allows us to consider more complex situations, particularly related to the dynamics of diversity.*

Figure 0.2: LBE Narbonne (France)

The reasons explained in the previous paragraph provide us with a few examples which explain why we are so interested in studying chemostat models, particularly by introducing some stochastic or random disturbances since these kinds of terms will allow us to obtain much more realistic mathematical models reflecting in a very loyal way what happens in laboratories when displaying the biological devices. Such a

great interest in considering stochasticity and/or randomness in the chemostat model is, amongst other motivations, due to the fact that stochastic differential equations jointly with the recent theory of dynamical systems are at its peak in the late years, for instance, because of their large number of interesting applications that can be found in every experiment concerning the real life.

Biological aspects

A bioreactor is an experimental device which is essentially an enclosure containing a nutrient medium consisting of a cocktail of various molecules, referred to as substrates, upon which one or more populations of microorganisms grow, and as such the set of these microorganisms is called biomass. Since biomass is the catalyst for reaction, the effectiveness of a biological system will be all the more significant when the substrate necessary for its growth is in an appropriate from, this is referred to as biodegradability, and accesible, so-called accessibility. The homogeneity of the medium as well as biomass and resource densities will consequently play essential roles in the operation of these systems. It may happen that the limiting resource in the feed may not be accessible to microorganisms, for example because it is found in solid form. In this case, it is necessary to add a hydrolysis step describing the manner how, velocity and yield depending on the conditions of the medium, this matter compartment feeds a biodegradable and accessible substrate compartment. In addition, we will assume that, apart from the nutrients, the other elements which are also essential for the growth and the development or reproduction of the species inside the reactor are present in excess at all times. Keeping these general points in mind, let us now focus on modeling a simple biological reaction.

Figure 0.3: Real bioreactors in LBE

Bioreactors are used to perform operations for transforming matter through biological pathways, most often accompanied, but not systematically, by the increase of biomass in the reaction medium. Attending to the way in which the nutrient is supplied from the feed bottle to the culture vessel, engineers establish the following classification of bioreactors:

- **Continuously-fed systems or chemostat.** The main characteristic in continuous reactors is that the reaction volume remains constant due to the fact that both input and output flow rates are identical. *It is the most commonly used operating mode in industries aiming to process a large amount of material arriving continuously, as it is the case, for example, in the treatment of water by biological means. It is one of the most significant for industries in terms of quantities of processed materials*. This mode will be our object of study in this dissertation because of its importance and applicability in the real life.

- **Semi-continuous or fedbatch.** This kind of bioreactors are mainly characterized by having no output flow. *In such a system, the reaction volume is thus increasing over time from a minimal to a maximal value. This type of system is particularly suitable for the production of biomass as the amoun of substrate can be supplied according to the specific need of microorganisms. It is also used when the risk of inhibition due to the substrate accumulation or a metabolic intermediary in the medium is present. Depending on the physiological state of microorganisms, it is then possible to decrease, or on the contrary, to increase the amount of the resource fed into the reactor.*

- **Batch mode or reactor.** Finally, this type of bioreactor refers to a closed system in the sense that there is neither supply nor withdrawal of the system. *In this kind of systems, substrates as well as biomass are introduced at the initial time. Therefore, the reaction volume of the system is constant over time and the reaction takes place up to the moment when it is measured, or considered, that it has completed. This operating mode is widely used in agri-food, pharmaceutical and chemical industries, notable for the production of molecules with high-added value, and more generally in cultures in which the risk of contamination through the feed is high.*

As explained before, this dissertation is dedicated to study the asymptotic behavior of the chemostat model. Then, in order to make the readers as much familiar as possible with the chemostat device, we will explain in more details its functioning from a biological point of view in the sequel.

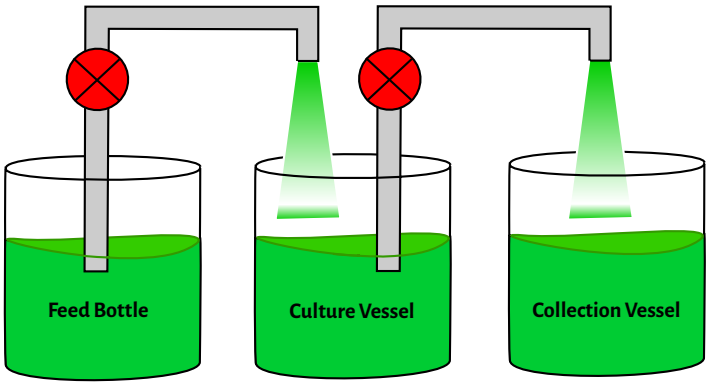


Figure 0.4: The simplest chemostat device

The simplest chemostat device consists in three different tanks called *feed bottle*, *culture vessel* and *collection vessel*, respectively, which are interconnected by pumps (see Figure 0.4) such that the nutrient is continuously supplied from the first tank to the culture vessel, and there is also another flow being pumped from the second tank to the collection vessel in order to remove excess material in the culture vessel, where the interactions between the substrate, or nutrient, and the microorganisms take place. In addition, some hypotheses are usually taking into account when studying chemostat models, for instance, the content in the culture vessel is assumed to be perfectly homogeneous and its volume is constant. These assumptions can be easily managed by using appropriate technical devices which allow us to maintain continuous and identical input and output flows.

Setting up the mathematical model

Once presented the chemostat device as well as the main ingredients regarding its biological aspects, in this section we state the equations which govern its behavior. To this end, we firstly specify a few conventions concerning the notation which will be used through the rest of the dissertation. Since the chemostat is a system consisting in an enclosure as well as two supply and withdrawal devices notable, including pumps that allow the user to set input and output rates, it then becomes possible to identify variables allowing us to interact with the system. These variables are precisely the microbial biomass, microorganisms or species, which will be denoted by x and the nutrient or substrate necessary for the growth of the species, which will be denoted by s. We would also like to remark that both state variables refer to the microbial biomass or the substrate, respectively, as well as their respective concentrations which are measured in mass per unit volume.

In order to establish the equations of the chemostat, we use here the usual formality of process engineering by directly applying a mass balance to x and s. Consider an enclosure of volume v equipped with an inlet, the supply of the reactor, and an outlet through which the reaction mixture can be withdrawn. To be as much formal as possible, we assume that this facility is equipped with all the necessary control devices so that the mixture is homogeneous. In addition, it is also assumed that from a reactive point of view, environmental conditions, such as temperature or pH are constant, in the sense that they are not the reason for the variations observed in concentrations of interest.

From now on, s_{in} will denote the concentration of the substrate in the feed bottle, q_{in} and q_{out} the input and output flow rates in volume per unit of time, respectively, and $y(\cdot)$ the yield of the conversion of substrate and biomass in mass of substrate consumed per mass of biomass produced. In the great majority of articles available in the literature, yields are constants. Now, we will focus our work on the dynamics of the state variables x and s. *Let us achieve a mass balance according to which, for a period of time dt, the variation in the mass of an element, here x and s, is the result between the mass of that element has been brought into the system added to the produced mass of this element minus the consumed quantity minus the extracted quantity. If this principle is applied to the biomass and to the substrate in the reaction volume v of the reactor, the following equations are obtained*

$$\begin{aligned}
\frac{dv}{dt} &= q_{in} - q_{out} \\
\frac{d(sv)}{dt} &= q_{in}s_{in} - q_{out}s - \frac{\rho(\cdot)}{y(\cdot)}v, \\
\frac{d(xv)}{dt} &= \rho(\cdot)v - q_{out}x,
\end{aligned}$$

where $\rho(\cdot)$ denotes the velocity or rate reactions by means of which the substrate is transformed into growth.

Without loss of generality, we will of course be cautious to only consider rates q_{in} and q_{out} that maintain v positive. Noting that

$$\frac{d(uv)}{dt} = u\frac{dv}{dt} + v\frac{du}{dt},$$

we can express the dynamics of the concentration of x and s that are more easily manipulated in chemistry than masses inasmuch as it is desirable to reason regardless of the volume of the reactors. It thus yields

$$\begin{aligned}
\frac{dv}{dt} &= q_{in} - q_{out} \\
v\frac{d(s)}{dt} &= q_{in}s_{in} - q_{in}s - \frac{\rho(\cdot)}{y(\cdot)}v, \\
v\frac{d(x)}{dt} &= \rho(\cdot)v - q_{in}x,
\end{aligned}$$

or still

$$\begin{aligned}
\frac{dv}{dt} &= q_{in} - q_{out} \\
\frac{ds}{dt} &= \frac{q_{in}}{v}(s_{in} - s) - \frac{\rho(\cdot)}{y(\cdot)}, \\
\frac{dx}{dt} &= \rho(\cdot) - \frac{q_{in}}{v}x,
\end{aligned}$$

Let us now define $\rho(\cdot) = \mu(\cdot)x$ where μ is called specific growth velocity. This assumption is reasonable since, having defined the biological reaction as being catalyzed by the presence of biomass, it simply guarantees that the growth velocity is zero in the absence of biomass.

This model is a means to obtain the equations of the dynamics of the substrate and the microbial biomass for all three models of operation of interest that we have previously outlined. However, since we will consider the chemostat model, by taking into account that $q_{in} = q_{out} \neq 0$ and denoting $D = \frac{q_{in}}{v}$, which is called the *dilution rate*, we obtain the following differential system

$$\frac{ds}{dt} = D(s_{in} - s) - \frac{\mu(\cdot)}{y(\cdot)}x, \tag{1}$$

$$\frac{dx}{dt} = -Dx + \mu(\cdot)x. \tag{2}$$

Concerning system (1)-(2), we easily recognize in each equation a term related to hydrodynamics, such as the transportation terms $-Dx$ and $D(s_{in} - s)$, and the reaction terms $\mu(\cdot)x$ and $-\frac{\mu(\cdot)}{y(\cdot)}x$. Finally, we will make another simplification which allows us to obtain the so-called *minimal model*. This model is called minimal because there would be nothing left of what characterizes a *real* chemostat if we tried to simplify it slightly more. For this model, we assume that $s \mapsto \mu(s)$ is a function only of the substrate such that it is zero at zero and that the yield $y(\cdot) = y$ is constant. Hence, it is not difficult to check that we can take $y = 1$

in (1)-(2) since, by performing the variable change $\bar{x} = x/y$ in (1)-(2), we can obtain the following equations

$$\begin{aligned} \frac{ds}{dt} &= D(s_{in} - s) - \mu(s)\bar{x}, \\ \frac{d\bar{x}}{dt} &= -Dy\bar{x} + \mu(s)\bar{x}, \end{aligned}$$

such that we have

$$\frac{ds}{dt} = D(s_{in} - s) - \mu(s)x, \tag{3}$$

$$\frac{dx}{dt} = -Dx + \mu(s)x. \tag{4}$$

As a result, this trick allows us to remove a parameter and, therefore, to obtain a simpler model to be studied. Henceforth, model (3)-(4) will be called *the chemostat model*.

In the previous part of the current section, *we have presented a model describing the dynamics according to which matter is transformed by biological means. However, we have not discussed the way in which the velocity, or kinetics, of the reaction can be modeled. The only assumption that has been made so far is that velocity ρ was written $\rho(\cdot) = \mu(\cdot)x$. Monod, in his works on the growth of microorganisms, discovered that the function $\mu(\cdot)$ only depended on the concentration of the limiting substrate. In particular, he introduced the function*

$$\mu(s) = \frac{ms}{a+s}, \tag{5}$$

see [66]. This function is zero for $s = 0$ and tends toward m when the substrate concentration becomes large compared to a. In addition, he named m the maximal consumption rate or the nutrient, and also the maximal specific growth rate of microorganisms, and a the semi-saturation constant. When $\mu = \mu(s)$, the growth rate is proportional to the population density. Nonetheless, this expression has given rise to numerous discussions. The first criticism that can be made of this expression is that it does not originate from a law, even if it is sometimes presented and named as such, but from a heuristic approach enabling a two-variable function to replicate data in a satisfactory way. In reality, it is inspired by the Michaelis-Menten expression established in 1913 and that which describes the kinetics of a reaction catalyzed by an enzyme, see [55]. The latter, even if it is not sufficient to describe complex situations, is based on mechanistic bases since a purely chemical formalism makes it possible to establish it. In the case of microbial growth, the situation is different because it is the product of a very large number of intracellular reactions whose result is observed at the population level. In more complex situations, the use of expressions involving a large number of parameters is necessary. We omit here the large number of expressions of the literature that have been proposed since Monod's time and we will merely identify the refinements that followed in microbial kinetics modeling.

It is essential to note here that in most cases, growth rate basically depends on a large number of parameters. For example, it is absolutely intuitive to consider that temperature and pH will play crucial roles in microbial growth: maintaining our refrigerator at four degrees makes it possible to limit the development velocity of microorganisms and as a result to preserve our food longer. In order to concentrate on the role of one or more limiting substrates, we

will consider here situations where these environmental variables will be, if not optimal, at least constant with values somehow ideal for microorganisms.

Up to now we have just mentioned the simplest deterministic chemostat model given by (3)-(4). Nevertheless, it is well known from biology that some species in the chemostat device tend to adhere to the walls of the culture vessel during the biological process. In order to model this natural situation and, therefore, to analyze more realistic chemostat models, which will be called from now on chemostat model with wall growth, we also state in this section the differential equations describing its dynamics. To this end, we firstly remark that they can be obtained in a similar way to the model without taking into account the wall growth, then we just focus on the terms which are new or different from the simplest case previously presented.

The deterministic chemostat model with wall growth is given by the following differential system

$$\frac{ds}{dt} = D(s_{in} - s) - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + bvx_1, \tag{6}$$

$$\frac{dx_1}{dt} = -(v+D)x_1 + \frac{cs}{a+s}x_1 - r_1x_1 + r_2x_2, \tag{7}$$

$$\frac{dx_2}{dt} = -vx_2 + \frac{cs}{a+s}x_2 + r_1x_1 - r_2x_2, \tag{8}$$

where s, x_1, x_2 denote concentration of the nutrient, the microorganisms in the liquid media and the ones sticked on the walls of the culture vessel, respectively. In addition, $b \in (0,1)$ describes the fraction of dead biomass which is recycled, $v > 0$ is the collective death rate coefficient of the microbial biomass representing all the aforementioned factors such as diseases, aging, etc. Apart from that, $0 < c \leq m$ is the growth rate coefficient of the consumer species. Finally, $r_1 > 0$ and $r_2 > 0$ represent the rates at which the species stick on to and shear off from the walls of the culture vessel, respectively.

We would like to mention here that this chemostat model with wall growth can be set up similarly to the case without taking into account the wall growth. The main difference is clearly that, in this case, we have two different species: the ones in the liquid media, denoted by x_1, and the ones sticked on the walls of the culture vessel, denoted by x_2. Because of this reason, we need a differential system of three equations. Concerning the equations describing the dynamics of the nutrient or susbtrate, (6), it is quite logical that we need here two terms concerning the consumption of the two different species. In addition, the term bvx_1 describes the microbial biomass which is recycled and hence can be considered as substrate. In (7), the term $-vx_1$ reflects the quantity of species which dies, $-Dx_1$ denotes the concentration of microbial biomass which is removed from the culture vessel to the collection vessel and, eventually, the last two terms just refer the quantity of microorganisms which stick on to and shear off the walls of the culture vessel. Finally, regarding (8), the only term which deserves to be mentioned, since the rest can be explained similarly as before, is the first one. In this case, we can observe that species are sticked on the walls of the culture vessel so they cannot be removed to the collection vessel hence we just write $-vx_2$ to take into consideration the microbial biomass death as a consequence of the biological process.

In the rest of the dissertation, we will analyze both chemostat models, the simplest one (3)-(4) and that which takes into account the wall growth (6)-(8), by introducing different kind of disturbances in each chapter. This will allow us to lead into new and more realistic models which will fit better the chemostat devices displayed in laboratories in the real life.

Some aspects already known about the simplest deterministic model

In this section some basic results concerning the simplest deterministic chemostat model will be presented in order to compare the differences between this model (3)-(4) and the ones studied along this dissertation when considering both stochastic or random terms. It will also make us easier to realize which ways of modeling stochasticity and/or randomness are more realistic.

On the other hand, the aim of this section is also to allow every reader to become comfortable with the results and knowledge already developed in the literature about the simplest deterministic chemostat such that it is easier to realize the achievements and contributions provided in this dissertation.

The following aspects are already known about system (3)-(4). We refer the interesting readers to [15, 49] for a more detailed information.

- **Existence and uniqueness theorem.** The theorem of existence and uniqueness of global solution can be easily proved by making use of the classical results concerning the theory of ordinary differential equations and thanks to the fact that the consumption function is continuously differentiable.

- **The horizontal axis defines an invariant set.** It can be trivially verified that for any initial value s_0 for the nutrient, the mapping

$$t \mapsto (s(t), x(t)) = (s_{in} + (s_0 - s_{in})e^{-Dt}, 0)$$

  defines a solution of system (3)-(4).

- **Positiveness of solutions.** We should remind that x and s denote quantities, or concentrations, which are positive or equal to zero. Thus, it is essential to be sure that every solution starting with positive initial conditions remains positive or equal to zero. In order to check this property, we just have to notice that, provided $s = 0$, we obtain

$$\frac{ds}{dt} = Ds_{in} > 0$$

  whence we deduce that no trajectory can leave the positive quadrant $\mathbb{R}^2_+ := \{(x, y) \,:\, x \geq 0,\, y \geq 0\}$ since, otherwise, it should cross the horizontal semi-axis which would contradict the uniqueness of solutions.

- **Another invariant set.** By defining the new state variable $z = s + x$, it is not difficult to check that

$$\frac{dz}{dt} = D(s_{in} - s) - Dx = D(s_{in} - (s + x)) = D(s_{in} - z)$$

holds, whence we can obtain its solution by integrating, which is given by

$$z(t) = s_{in} + ((s_0 + x_0) - s_{in})e^{-Dt}$$

for any initial pair $(s_0, x_0) \in \mathbb{R}^2_+$. Then, one can easily observe that z is approaching to s_{in} asymptotically which means that the segment

$$I = \{(s, x) \in \mathbb{R}^2_+ \,:\, s + x = s_{in}\}$$

is an attractive positively invariant set. Hence, if we restrict the dynamics of system (3)-(4) to this segment, we can replace s by $s_{in} - x$ such that equation (4) becomes the following differential equation

$$\frac{dx}{dt} = (\mu(s_{in} - x) - D)x,$$

whose behavior is completely known as soon as the graph of the mapping $x \mapsto \gamma(x) = (\mu(s_{in} - x) - D)x$ is known. In addition, the equality $s_{in} = s + x$ reflects the fact that the amount of consumed substrate is transformed into an equal amount of biomass as long as the yield is equal to one.

- **Boundedness of solutions.** It is automatically fulfilled by taking into account that mapping $t \mapsto z(t) = s(t) + x(t)$ is bounded and the fact that both state variables s and x take positive values or zero.

- **Equilibria.** It is easy to check that there exists a constant solution $(s_{in}, 0)$, which is called *washout* or *washed out* equilibrium and corresponds to a reactor without any microbial biomass. The rest of equilibria are given by (s^*, x^*), where s^* is a value such that $\mu(s^*) = D$ and $x^* = s_{in} - s^*$ hold.

In the rest of the section, we will assume that our growth function $\mu(\cdot)$ is Monod or, in other words, it is monotonic and bounded. Then, the first thing we would like to remark is the fact that, concerning the deterministic chemostat model (3)-(4), the term $\mu(s)$ in the equation for the substrate is a harvesting rate whereas the one appearing in the equation describing the dynamics of the species is a growth rate. In addition, we remark from the definition of the Monod function (5) that the larger the substrate concentration is, the more significant the specific growth velocity of microorganisms is as well.

By considering the Monod function as explained in the previous paragraph, we know that two different equilibria arise. On the one hand, the washout equilibrium which is given by $(s_{in}, 0)$. On the other hand, let us define the constant λ_D as the unique value of the substrate concentration such that $\mu(s) = D$ holds true, as long as $D < m$ is fulfilled. Hence, it is straightforward that the growth velocity of the microbial biomass is strictly negative if $s < \lambda_D$ whereas it is strictly positive when $s > \lambda_D$

is fulfilled. Because of this reason, the constant λ_D is called the *break-even concentration*. Let us define now $s^* = \lambda_D$ and $x^* = s_{in} - s^*$. Then (s^*, x^*) is an equilibrium with positive biomass which is globally asymptotically stable as long as $D < \mu(s_{in})$ holds true, which means persistence of the microbial biomass. Nevertheless, if $D \geq \mu(s_{in})$ the washout equilibrium $(s_{in}, 0)$ becomes globally asymptotically stable, then the species becomes extinct.

Organization and contributions of the dissertation

As mentioned previously, this dissertation is dedicated to model and analyze different chemostat devices affected by some stochastic and/or random perturbations. It is well-known that there exist many different ways of modeling stochasticity and/or randomness in some deterministic system, see [5–7, 42, 53, 74–76, 79, 80]. Nevertheless, there are also many questions to be taken into account as a first step, for instance, we could think about the following topics:

- **Which kind of stochastic/random perturbation can we introduce?** There are many different stochastic processes and we need to make a decision in order to set up our stochastic/random model. Particularly, in this dissertation we will consider the standard Wiener process in the first and the third chapters, the Ornstein-Uhlenbeck process in the second chapter and the fractional Brownian motion in the fourth one.

- **How can we do it?** Once decided the stochastic process to perturb the system, we need to think where and how we can introduce the disturbances. For instance, in the first two chapters of this dissertation we perturb the dilution rate, or its corresponding input flow, motivated by some personal discussions with biologists and other researchers who are experts on the chemostat model whereas, in the last two chapters, we perturb the corresponding deterministic systems in a different way to model, for instance, environmental effects. We remark that each different way to perturb the original deterministic models will be properly motivated in the corresponding chapters.

- **Is it realistic from the biological point of view?** After thinking about the previous questions, we should think whether our resulting stochastic/random model is realistic in order to obtain models which reflect the reality as much better as possible. To this end, it could be interesting to make some numerical simulations in order to decide if the stochastic process, and of course the way in which it has been introduced, reproduce what we expect from the reality in an appropriate way. Even though the numerical simulations are usually made after finishing the mathematical study in order to support the results provided previously, it is also very important to try some preliminary ones when deciding the kind of disturbances which can be introduced since it helps us to obtain much more realistic systems.

- **And last but not least... is it tractable from the mathematical point of view?** Of course, we need our models to be as much realistic as possible but we also need to have some tractability in order to make calculations, since no work could be made otherwise. Sometimes one can found some models which reflect very well the real devices in a really broad sense but the model is so complicated to deal with

that either it is not possible to analyze its equations or just little comments can be said. Due to this facts, we need to find some suitable balance which will make our work both tractable and realistic and, then, original and interesting.

After thinking carefully about these questions, we will analyze in this dissertation the effects of different types of noise and different ways of introducing stochasticity and/or randomness in the deterministic chemostat models given by (3)-(4) as well as (6)-(8).

In **Chapter1**, the effects caused by the standard Brownian motion in the chemostat model are analyzed. Particularly, we are interested in introducing some disturbances on the input flow or, equivalently, in the dilution rate such that the parameter D is perturbed as $D+\alpha\dot{W}(t)$, where $W(t)$ denotes a standard Wiener process and $\alpha \geq 0$ represents the intensity of the noise. The resulting stochastic system without taking into account the wall growth is understood in Itō sense, is given by

$$\begin{aligned} ds &= \left[(s_{in}-s)D - \frac{msx}{a+s}\right]dt + \alpha(s_{in}-s)dW(t), \\ dx &= x\left(\frac{ms}{a+s} - D\right)dt - \alpha x dW(t), \end{aligned}$$

and has already been analyzed in [77] by using the classical techniques from stochastic analysis and some stability results are provided there. Nevertheless, as in our opinion there are some unclear points in the analysis carried out there, our aim in this chapter is to use an alternative approach to this problem, specifically the theory of random dynamical systems, which will allow us to partially improve the results in [77]. In addition, we will provide some results which hold almost surely while those in [77] are just said to hold *in probability*.

In this chapter both stochastic chemostat models with and without wall growth will be considered after introducing the disturbances explained in the previous paragraph. In both cases, a suitable variable change involving the Ornstein-Uhlenbeck process (see Appendix A for its definition) will be performed in order to transform our original stochastic system into a random one which will be much easier to deal with. After that, the existence and uniqueness of global solution will be stated just like that the generation of a random dynamical system, which will be an essential ingredient henceforth. Thanks to that, the existence of a tempered compact random absorbing set will be stated which will allow us to ensure the existence and uniqueness of a random pullback attractor associated to the random chemostat model. Moreover, we will go further by analyzing in more detail the differential equations which govern the nutrient and the microbial biomass individually, obtaining some results concerning the internal structure of the corresponding random pullback attractor. Thanks to this deeper analysis we will provide interesting results concerning the asymptotic dynamics of our system. Then, a conjugation lemma will be used to obtain the random dynamical system associated to the original stochastic chemostat model as well as its corresponding random pullback attractor. Finally, several numerical simulations will be shown to support the theoretical results proved along the whole chapter, providing also the numerical scheme used to make them, which will be considered in the following chapters as well.

From the previous analysis, some drawbacks can be found. On the one hand, one can observe that some state variables can take negative values which does not produce any mathematical inconsistence in our analysis or, in other words, our mathematical analysis is accurate to handle the mathematical problem. Nevertheless, from the biological point of view, this may reflect some troubles since it would mean that there is some reverting flows in the pumps which would be totally unrealistic. As a consequence, this problem suggests that either the fact of perturbing the dilution rate with an additive noise may not be a realistic situation, or that we should try to use another different approach when modeling disturbances in the input flow of the chemostat device.

Considerations of stochastic processes in the chemostat model have already been tackled in the literature, but mainly on the growth function (see [9,10,13]). This appears particularly relevant when the number of individual bacteria could be small, with a risk of extinction of the biomass populations in finite time. Nevertheless, sudden extinction in continuous cultures that are well supervised about a nominal regime are quite rare in practice. On another hand, fluctuations on the input flow that brings permanently resources to the bacterial population in continuous cultures are much likely to be observed. Hence, in **Chapter 2** we will focus on the way to model these random fluctuations, taking into consideration that the effective flow rate has to stay non-negative and taking also into account the wall growth in a second part. From the biological point of view, the fact of introducing a noisy term in the input flow of the chemostat models is a really interesting problem found in the laboratory since, for instance, it reflects the presence of particles of dirt inside the pumps or temporary clogs at the input or output of the chemostat. Then, it is well known that continuous flows are often subjected to random fluctuations with time.

Thus, in this chapter we will consider a suitable Ornstein-Uhlenbeck process to perturb the dilution rate in both chemostat models, with and without wall growth. Particularly, we are interested in perturbing D by the random term $D + \alpha z^*_{\beta,\nu}(\theta_t\omega)$, where $z^*_{\beta,\nu}(\theta_t\omega)$ denotes some suitable O-U process, which will be carefully introduced in Section 2.1, and $\alpha > 0$ represents again the amount of noise. The parameter β appearing in the O-U process will allow us to bridge a gap between a pure standard Wiener process and no noise at all. In addition, the value of such parameter is related to the amplitude of the deviations observed on the realizations.

In the sequel, we will just refer to the chemostat model without wall growth in order to motivate the study carried out in this chapter since the same arguments are valid for the motivation of the one with wall growth, which will be also analyzed in this chapter as well.

In such a way, the resulting random chemostat model without wall growth is given by the following system of differential equations

$$\begin{aligned} \frac{ds}{dt} &= (s_{in} - s)\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right] - \mu(s)x, \\ \frac{dx}{dt} &= -\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right]x + \mu(s)x. \end{aligned}$$

Concerning the O-U process, some essential properties will be provided in Section 2.1 which will allow us to set up a new framework and, moreover, to make calculations in the next sections. To sum up some of the main ingredients to be used, for every fixed event ω, it will be possible to choose $\beta_\omega \in \mathbb{R}$ such that the corresponding realizations of the perturbed input flow, $D + \alpha z^*_{\beta_\omega,\nu}(\theta_t\omega)$, will remain for every $t \in \mathbb{R}$ inside some strictly positive band which should be previously fixed, for instance, by practitioners. In such a way, for every fixed event ω, the resulting random chemostat model will be given by

$$\frac{ds}{dt} = (s_{in} - s)\left[D + \alpha z^*_{\beta_\omega,\nu}(\theta_t\omega)\right] - \mu(s)x, \tag{9}$$

$$\frac{dx}{dt} = -\left[D + \alpha z^*_{\beta_\omega,\nu}(\theta_t\omega)\right]x + \mu(s)x. \tag{10}$$

As a consequence, since $\beta_\omega \in \mathbb{R}$ depends on the event ω previously fixed, the solutions of system (9)-(10) may not generate a random dynamical system. Nevertheless, this does not represent any inconvenient for the analysis of the long time behavior of the random differential system (9)-(10), since it can be investigated for every fixed event ω. In fact, we will be able to obtain some results on forwards convergence (in time) of solutions, instead of the pullback convergence ensured within the framework of random dynamical systems.

This new approach, which arises from the nature of the particular noise (the suitable O-U process), leads into another unusual technique which seems to be really interesting since, for instance, allows us to guarantee the existence of compact and attracting sets which are strictly positive, whence we will ensure the persistence of the species in the sense that there exists a number $\eta > 0$ such that, for any non null initial biomass $x(0)$, each realization satisfies

$$\liminf_{t\to+\infty} x(t) \geq \eta > 0. \tag{11}$$

Needless to say that this is the principal goal pursued by biologists, differently to other several previous works as [53], where the authors consider disturbances in the chemostat model by means of the standard Wiener process, and prove some results concerning the persistence of the microbial biomass in the sense $\liminf_{t\to+\infty} x(t) > 0$, which is clearly weaker than (11).

We will also achieve some improvements comparing our results throughout this chapter with the ones by Xu *et al* in [77] since, even though they consider stochastic noise on the dilution rate in the chemostat model, they need a condition on the parameter of the amplitude of the noise to ensure the persistence of the species (see, for instance, Theorem 1.2 and Section 4 in [77] where the authors ensure the necessity of a smallness condition on the amount of noise $\alpha > 0$) whereas, in our case, modeling the disturbances with the Ornstein-Uhlenbeck process, there is no discussion needed on the amplitude of the noise to ensure the persistence, which is in addition in the stronger sense (11). Moreover, the authors in [77] say to prove the results *in probability* while we will prove all the results almost surely, i.e., for every realization in a set of events of full measure.

Apart from that, we would like to remark that some improvements are also obtained when comparing our results (and of course the way of modeling) with the ones in [16]. In that paper, the authors analyze some similar random disturbances on the input flow in the chemostat model, with and without wall growth, such that they replace D by $D(\theta_t\omega)$ and, then, they prove the existence and uniqueness of a random pullback attractor by assuming that $D(\theta_t\omega)$ remains bounded inside a positive interval for all $t \in \mathbb{R}$. We highlight that our analysis in this dissertation significantly differs from the one carried out in [16] since, there, the resulting random systems generate a random dynamical system and, therefore, the authors can apply the techniques involving pullback random attractors. However, we recall that our systems in Chapter 2 may not generate a random dynamical system but we can analyze the long-time behavior of the corresponding models without any inconvenient. In fact, this new approach allows us to prove the existence of attracting sets which are deterministic and, what is more, they are obtained in forward sense. Another significant difference between the work made in [16] and the one carried out in the second chapter of this dissertation is that, in our case, we know explicitly how the realizations of the perturbed dilution rate are.

The previous reasons constitute a few representative examples which support that this way of perturbing the dilution rate by using the Ornstein-Uhlenbeck process fits much better the real situations we wish to model. Apart from the advantages described above, we will also obtain some improvements with respect to results obtained when analyzing the deterministic chemostat model (3)-(4), as we will explain in more detail in Chapter 2. To be more precise, in the deterministic setting the washout equilibrium $(s_{in}, 0)$ is attractive if $D = \mu(s_{in})$ whereas, in our case by using the O-U process, it is possible to prove that there exists a deterministic attracting set (forwards in time) for the solutions of our system, which has several points (in fact, all of them except to the washout) inside the positive cone. Finally, we will also show several numerical simulations which will support the results previously proved. Thanks to that, we will be able to observe again the great advantages of using the Ornstein-Uhlenbeck process when modeling stochasticity and randomness in the input flow of the chemostat model.

In view of that, we are really encouraged to think about revisiting the persistence of species under input disturbances in case, for instance, of competition between several species. In fact, as we will explained at the end of this introductory chapter, this research line is one of our main interests now.

In **Chapter 3**, we will perturb both chemostat models, the simplest one as well as the one with wall growth, by means of the standard Brownian motion again. Nevertheless, differently to Chapter 1 where some drawbacks were found, in this chapter we will use a technique based in the one carried out by Fudenberg and Harris in [36], by Foster and Young in [34] or in [53] by Imhof and Walcher, which ensures the positivity of both the nutrient and the microbial biomass, although does not preserve the washout equilibrium from the deterministic to the stochastic model. More precisely, we will be interested in analyzing the following system understood in Itō sense

$$ds = \left[(s_{in} - s)D - \frac{msx}{a+s}\right]dt - \alpha s dW(t), \tag{12}$$

$$dx = \left[-Dx + \frac{msx}{a+s}\right]dt - \alpha x dW(t), \tag{13}$$

where $W(t)$ is a standard Brownian motion and $\alpha \geq 0$ represents the intensity of the noise.

We remark that, in order to make the calculations more tractable and clear, we will consider the same noise in both equations, even though a similar analysis could be developed by using different Brownian motions in each equation.

Now, we would like to highlight some significant insights discovered throughout this work. We will only refer to the case without wall growth since similar ones hold for the other case as well.

Concerning the deterministic chemostat model (DCM) given by (3)-(4), some authors have recently proved (see [15–17]) the existence of a unique axial equilibrium $(s_{in}, 0)$, the also called washout, which is asymptotically stable provided $D > m$, therefore this situation corresponds to the extinction of the microorganisms. However, if $D < m$ and $aD/(m-D) < s_{in}$ the washout equilibrium becomes unstable and a unique positive globally asymptotically stable equilibrium appears inside the positive quadrant, i.e., persistence of the microorganisms can be ensured. Notice that, in this case, the global attractor exists and consists of both equilibria and the heteroclinic solutions between them. Otherwise, no more information can be deduced related to the asymptotic behavior of the system.

Regarding the stochastic chemostat model (SCM) given by (12)-(13), we will prove in this chapter that there exists a unique global random attractor which is given by the singleton components $(s_{in}D\rho^*(\omega), 0)$ provided $D + \alpha^2/2 > m$, see Section 3.1.3 in Chapter 3 for more details. Otherwise, the unique global random attractor is contained in a segment whose intersection with the axes $s = 0$ and $x = 0$ is reduced to two singleton points.

In light of the previous facts, observe that when $D < m$ and $aD/(m-D) < s_{in}$ we can choose α large enough such that $D + \alpha^2/2 > m$. This means that persistence of the microorganisms holds for (DCM), while for (SCM) we have extinction since the pullback random attractor becomes the single random point $(s_{in}D\rho^*(\omega), 0)$. This fact is closely related to the stabilizing effect that Itō's noise can produce on deterministic systems. However, if we considered a Stratonovich interpretations for our perturbation at the beginning of our study, then we would have obtained D instead of $D + \alpha^2/2$ in the corresponding stochastic system; in other words, assumption $D + \alpha^2/2 > m$ in (SCM) would become $D > m$, the same that we had for (DCM). Consequently, no stabilizing effect is produced by the noise (see [15, 20, 51] and Remark 3.3 in [56] for a more detailed discussion on this topic). Thus, not only the type of noise but also its mathematical interpretation can provide different results, something that has to be taken into account by the modeler. A reference that could help to make the appropriate choice in a specific application is [73], where the author presents a criterion for determining which interpretation of the noise is the most useful in his work.

Finally, we would like to introduce in both deterministic chemostat models, with and without wall growth, a new stochastic process which is becoming lately more and more popular between researchers from many areas: the fractional Brownian motion. Even though every detail about this new noise and its several advantages will be explained in **Chapter 4**, where the corresponding stochastic models will be carefully investigated, we would also like to mention in this introductory chapter some of them to motivate its study.

The fractional Brownian motion (fBm) is a centered Gaussian process B^H indexed by the Hurst parameter $H \in (0,1)$. This stochastic process, which is in addition self-similar and it is characterized by the stationarity of its increments, was introduced by Kolmogorov in 1940 (see [57]) to study the long term storage capacity of reservoirs along the Nile river. This kind of noise provides us a very good candidate to model random long-time influences in climate systems, hydrology and medicine, between others, specially in the case $H > 1/2$, as will be considered in this dissertation, since it satisfies a long-memory property then. In addition, the fBm coincides with the standard Brownian motion when $H = 1/2$.

Differently to the standard Wiener process, the fBm is neither a martingale nor a Markov process when $H \neq 1/2$. Because of that, we cannot use the Itō's theory to define the stochastic integral with respect to the fBm, hence it is necessary to set up a new theory to define that integral. To this end, two possibilities are available: on the one hand, we can use the so-called *rough path theory* which defines the corresponding integral as a point-wise limit (see [35, 64]); on the other hand, we can use the *fractional calculus theory* which replaces the usual ordinary derivatives by suitable fractional derivatives using its Weyl representation (see [38,43,44,65,68,72]). We will focus on this latter situation which will allow us to define the stochastic integral with respect to the fBm as a generalized Riemann-Stieltjes integral, which is called the *path-wise theory*. For more detailed information about this approach, we recommend every interested reader to see the pioneer works of Zähle (see [78]), Decreusefond and Üstünel (see [29]) and Lyons (see [63]).

We would like to note that the modern theory of random dynamical systems, which is the base of this dissertation, still works even though the fBm and the stochastic equations driven by them do not generate a Markov process, as we will see in the last chapter. In addition, we would like to remark that many papers in the literature treat pullback attractors for stochastic differential equations driven by a fBm with $H > 1/2$. Nevertheless, the authors usually assume that the diffusion coefficient has a very particular form, for instance, it is additive (see [28, 29]), multiplicative (see [69]) or other special cases (see [32]). In the previous cases, these particular forms allow the authors to make use of a cohomology method which transforms the original stochastic system into a random one with random parameters. However, in this dissertation we will deal directly with the stochastic chemostats driven by fBm, even though our diffusion term is linear (we notice that this work is an extension of the previous chapters where the same model, but affected by a standard Brownian motion, was considered). Thanks to that, we will be able to analyze other more sophisticated systems with more general diffusion coefficients with no extra work.

Once introduced the new framework to deal with the fBm, in Chapter 4 the fractional Brownian motion will be presented as well as the main concepts needed to deal with the corresponding stochastic system such as the fractional derivative and the fractional integral. We will also provide some basic results concerning the integral with respect to the fBm which will be essential henceforth. In order to analyze this new stochastic system, which will be given by

$$\begin{aligned} ds &= \left[(s_{in}-s)D - \frac{msx}{a+s}\right]dt + \alpha s dB^H(t), \\ dx &= \left[-Dx + \frac{msx}{a+s}\right]dt + \alpha x dB^H(t), \end{aligned}$$

we will write the model in its abstract form

$$du = (Au + F(u))dt + G(u)dB^H(t)$$

such that we will just analyze the case without taking into account the wall growth (the case with wall growth can be studied analogously). The existence and uniqueness of global solution in some suitable damped Hölder space will be stated as well as the generation of a random dynamical system. Our aim in this chapter, similarly to the previous ones, is to prove the existence of a tempered compact random absorbing set since, thanks to that, we will be able to guarantee the existence and uniqueness of random pullback attractor. Nevertheless, some significant differences can be found in this case since we have to deal with the noise explicitly. Because of this fact, we will introduce a sequence of stopping times which will help us to control, in some sense, the size of the noise and will allow us to obtain a discrete tempered absorbing set associated to a new discrete random dynamical system which will be defined, in rough words, as the restriction of the original continuous one to the sequence of stopping times. Thanks to some suitable discrete Gronwall lemma, we will be able to guarantee the existence and uniqueness of a discrete random pullback attractor whence we will deduce the existence and uniqueness of the continuous one as well. Finally, we will also show some numerical simulations which will allow us to observe how the realizations of the solutions of our system affected by the fractional Brownian motion are.

We would like to remark here that the results and techniques developed through this chapter are just a first approach to the fractional Brownian motion. Our aim is to check that the chemostat models treated in this dissertation can be also perturbed by such a new noise and similar results to the ones provided in the literature for general stochastic differential equations can be obtained. Nevertheless, there are several new research lines which merge from this initial work, as will be detailed at the end of this introductory chapter.

Different appendices can also be found at the end of the dissertation concerning some basic concepts regarding the theory of random dynamical systems as well as some preliminaries on stochastic processes and their properties. Apart from that, for the sake of readability, a brief appendix containing some technical results which are used when investigating the chemostat models affected by fractional Brownian motion in Chapter 4 can be found in order not to make the arguments given in the corresponding chapter confusing.

Current and future research lines

As already explained, there are many interesting facts which could be investigated concerning the chemostat model because of the large variety of interesting applications that it has in the real life. This is the reason which encourages us to continue working on this model and, due to that, we will summarize in the following paragraphs some ideas that we consider really interesting, some of them are currently part of our daily working routine.

Chemostat with fractional Brownian motion. One could wonder why only one chapter is dedicated to fractional Brownian motion when the title of this dissertation includes such noise. In fact, before studying the fractional Brownian motion with $H \neq 1/2$, it was necessary to complete the analysis for the case $H = 1/2$, which is also fractional. Thus, as explained before, Chapter 4 just consists on a first approach to model stochastic chemostat by means of the fractional Brownian motion. Nevertheless, there are many works to do henceforth, for instance, it would be interesting to obtain some detailed about the internal structure of the random pullback attractor. Another approach could be to investigate the stability of the trivial solution of the corresponding stochastic system with fractional Brownian motion. Finally, we would like to remark that we analyze a chemostat model where the stochastic diffusion terms is given by $G(u) = \alpha u$ since it consisted on an extension of the models studied in the previous chapters. However, as long as the diffusion term satisfies some properties as in this case, other kinds of diffusion terms could be consider, in fact, this is the main advantage of using the fractional Brownian motion against the standard Wiener process.

Competition of several species. In this dissertation we will focus on two different chemostat models, as explained before. On the one hand, we will study the growth of a single species of microorganisms on a resource. On the other hand, we will also focus our attention in studying the corresponding chemostat model by taking into account the wall growth as well since it is a natural fact which takes place in the laboratory as soon as you set up a chemostat device or, in general, some devices involving biological processes. Nevertheless, when taking into account the wall growth, we consider that both microorganisms, the ones in the liquid media and the ones sticked on the walls of the culture vessel, have the same consumption function.

In view of this fact, it could be also very interesting to analyze a chemostat model with two different species, i.e., by considering two different consumption functions. We are currently working on this topic by using the techniques developed in Chapter 2, i.e., by perturbing the input flow by means of the Ornstein-Uhlenbeck process and we hope to obtain again the existence and uniqueness of a strictly positive random attractor which allows us to guarantee the persistence of the species, of course, under some condition on the parameters involved in the system.

Different consumption functions. We would like to remark that the analytic expression of the consumption function, the Monod one in this dissertation, is just an approximation coming from data in the laboratories. Nevertheless, we could consider different consumption functions involving different kinetics such as Haldane or Contois functions, to name the most common ones apart from the Monod. Let us motivate the use of this new functions as follows.

If a substrate is limiting at low concentration, it can also prove toxic when its concentration becomes significant in the medium. In 1968, see [2], Andrews suggested an expression for $\mu(s)$ involving three parameters to describe the growth rate of a microorganism limited by a low concentration of substrate but inhibited when

the concentration becomes significant (see [46]). This function is written

$$\mu(s) = \mu_0 \frac{s}{s + K_s + \frac{s^2}{K_i}},$$

where μ_0 and K_s are, respectively, the maximum growth rate and the semi-saturation constant in the absence of inhibition and K_i the inhibition constant. We will see that the choice of this kinetics leads to very significant changes in the qualitative properties of biological models. It is particularly interesting to note here that this function actually describes an indirect inhibition phenomenon. Similarly to the Monod equation, this equation is not a law of nature but expresses the fact that at high concentrations, the complex mechanisms involved in fact cause a change of pH and that it is this variation of pH which has, in fine, a consequence on growth. The Haldane function thus perfectly illustrates the manner in which very complex phenomena can be reduced to simple modeling by adopting a macroscopic point of view at the population level.

It is not difficult to observe that the previous consumption functions just depended on the substrate density. Nevertheless, some authors propose another one depending not only on the substrate density but also on the biomass one, motivated by the fact that data coming from complex microbial ecosystems in mixed cultures are much better reproduced by using this kind of kinetics. The so-called Contois function is defined as

$$\mu(s, x) = \mu_{max} \frac{s}{s + K_s x},$$

whose main characteristic is that it decreases as soon as the biomass density increases. This consumption function is also called ratio-dependent since it can be written as

$$\mu\left(\frac{s}{x}\right) = \mu_{max} \frac{\frac{s}{x}}{\frac{s}{x} + K_s}.$$

Similarly to the previous case of inhibition, this function is very helpful when it comes to account for complex aggregation phenomena such as biomass structuring in flocs. In effect, in this case, the part of biomass that is located in the core of the flocs receives the substrate by diffusion only, hence a strong limitation of growth. It follows that at a given microbial population, the overall growth is lower in comparison to a situation in which biomass would not be structured into flocs, see [45, 48, 59].

Flocculation. It is well-known that microorganisms tend naturally to agglomerate in biofilms and flocs. Then, instead of studying the chemostat model by considering just planktonic microorganisms, an interesting approach could be to take into account the flocculation or, in other words, the structuring of the microbial biomass into flocs.

Spacialization. Up to now we just considered bioreactors which were perfectly homogeneous. However, it is totally logical to question this homogeneity property specially when working with reactors whose volume is considerably large. *In addition, if we broaden the formalization field of the chemostat to the description of natural ecosystems, then there are many situations in which the structuring of the natural space can be seen as more or less large volumes connecting each others by flows of matter and/or energy.*

If we have a perfect knowledge of the dynamic behavior of each individual entity, the interest in formalizing this natural space as a network of interconnected chemostats is immediately understood. Note that if we consider flows of matter whose intensity can be varied going from a reactor A to a reactor B and vice-versa, we are confronted with a situation in which diffusion phenomena can be studied. The first configurations involving interconnected chemostats are known under the name of gradostat and have been proposed as early as the 1970s to simulate an environment where gradients of concentration of a limiting substrate can be observed as is often the case in a natural space (see [26, 61]). By adopting this approach, it is possible to represent numerous non-homogeneous situations by a network of interconnected reactors. The originality of these approaches is to avoid having to write partial derivative equations, which are more difficult to manipulate than a differential system even if the latter is of large dimension. It is also interesting to point out that if the biological part is forgotten, these approaches that consist of considering networks of reactors (these are then essentially cascades of reactors in which the output of one is the input of the other, which are studied) have been used in the 1950s to study flows in chemical reactors. In particular, these networks have been addressed precisely to approximate the hydrodynamic behavior of non-homogeneous reactors, also called plugflow reactors, which is one of the ideal reactors of process engineering (see [23–25]). In addition, such configurations have been proposed to bring forward ratio-dependent growths (see [3]) or still to model biofilm reactors (see [31]). In all these situations, the flow rates between the different chemostats of the networks under consideration are a priori constant. Already very rich in terms of dynamics, considering the chemostat or a network of chemostats in a context where flows that connect them vary opens very interesting new perspectives.

Applications to other models. Once finished this dissertation, we would also like to apply some of the techniques used here to other mathematical models, not necessary related to the chemostat device. Particularly, we are really interested in applying the idea developed in Chapter 2 to introduce randomness in other biological models by means of the Ornstein-Uhlenbeck process since we could obtain, as in the case of the chemostat, much more realistic systems which fit better the real models.

CHAPTER 1

Modeling and analysis of stochastic disturbances on the input flow in chemostat models

In this first chapter, the simplest deterministic chemostat model will be considered and the input flow will be perturbed by means of the classical standard Wiener process, which is also called Brownian motion or white noise, in order to model and analyze the environmental effects caused by a non-bounded noise. The existence and uniqueness of global solution of the corresponding stochastic models will be proved. After that, the positiveness of the unique global solution will be stated for every initial value in the upper-half plane. Furthermore, a random dynamical system will be defined by using the unique global solution such that the techniques and results of the theory of random dynamical systems will be used to guarantee the existence of an absorbing set which will allow us to ensure the existence and uniqueness of a random pullback attractor. In addition, we will be really interested in analyzing the internal structure of the so-called random pullback attractor since it will provide us further and more detailed information about the long-time behavior of our system and, therefore, the qualitative asymptotic behavior of the dynamics of both the nutrient and the species. Finally, we will show a Milstein scheme which will help us to obtain several numerical simulations to support the provided results through the whole chapter.

The results and explanations concerning the contributions of this chapter can be found in [9, 13, 60].

1.1 Stochastic chemostat model

Let us first recall the simplest deterministic chemostat model with Monod kinetics

$$\frac{ds}{dt} = (s_{in} - s)D - \frac{msx}{a+s}, \tag{1.1}$$

$$\frac{dx}{dt} = x\Big(\frac{ms}{a+s} - D\Big), \tag{1.2}$$

where $s(t)$ and $x(t)$ denote concentrations of the nutrient and the microbial biomass, respectively; s_{in} denotes the volumetric dilution rate, a is the half-saturation constant, D is the dilution rate and m is the maximal consumption rate of the nutrient and also the maximal specific growth rate of microorganisms. We notice that all parameters are positive and we use a function Holling type-II, which is defined as $\mu(s) = ms/(a+s)$, as functional response of the microorganism describing how the nutrient is consumed by the species (see [71] for more details and biological explanations about this model).

In order to obtain a more realistic model we will perturb the dilution rate, or its corresponding input flow, in (1.1)-(1.2) by means of a white noise. Let us recall that $D = q_{in}/v$, as explain in the introductory chapter, where q_{in} denotes the input flow rate and v the volume of the culture vessel. As v is constant in the chemostat device, it is equivalent to have disturbances on the dilution rate D instead of considering them on the input flow q_{in} To this end, we will replace D by $D + \alpha\dot{W}(t)$, where $W(t)$ is a white noise and $\alpha \geq 0$ represents the intensity of noise. Then, system (1.1)-(1.2) becomes the following system of stochastic differential equations understood in the Itō sense

$$ds = \Big[(s_{in} - s)D - \frac{msx}{a+s}\Big]dt + \alpha(s_{in} - s)dW(t), \tag{1.3}$$

$$dx = x\Big(\frac{ms}{a+s} - D\Big)dt - \alpha x dW(t). \tag{1.4}$$

System (1.3)-(1.4) has been analyzed in [77] by using the classical techniques from stochastic analysis and some stability results are provided there. However, as in our opinion there are some unclear points in the analysis carried out there, our aim in this chapter is to use an alternative approach to this problem, specifically the theory of random dynamical systems, which will allow us to partially improve the results in [77]. In addition, we will provide some results which hold almost surely while those from [77] are said to hold in probability.

Note that, thanks to the well-known conversion rule between Itō and Stratonovich formulations, we obtain from (1.3)-(1.4) its equivalent Stratonovich one given by

$$dS = \Big[(s_{in} - s)\bar{D} - \frac{msx}{a+s}\Big]dt + \alpha(s_{in} - s) \circ dW(t), \tag{1.5}$$

$$dx = \Big[-\bar{D}x + \frac{msx}{a+s}\Big]dt - \alpha x \circ dW(t), \tag{1.6}$$

where $\bar{D} := D + \frac{\alpha^2}{2}$.

1.1.1 Stochastic chemostat becomes a random chemostat

In this section we investigate the stochastic system (1.5)-(1.6). To this end, we first transform it into differential equations with random coefficients and without white noise by means of the following variable change which involves the stationary Ornstein-Uhlenbeck process denoted by z^* (see Appendix A).

$$\sigma(t) = (s(t) - s_{in})e^{\alpha z^*(\theta_t\omega)}, \tag{1.7}$$

$$\kappa(t) = x(t)e^{\alpha z^*(\theta_t\omega)}, \tag{1.8}$$

where ω denotes a standard Brownian motion and and $\theta_t\omega$ denotes the Wiener shift flow (see Appendix A for more information).

For the sake of simplicity we will write z^* instead of $z^*(\theta_t\omega)$, and σ and κ instead of $\sigma(t)$ and $\kappa(t)$.

On the one hand, by differentiation, we have

$$\begin{aligned} d\sigma &= e^{\alpha z^*(\theta_t\omega)}ds + \alpha(s - s_{in})e^{\alpha z^*(\theta_t\omega)}[-z^*dt + dW] \\ &= -\bar{D}\sigma dt - \frac{m(s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)})}{a + s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)}}\kappa dt - \alpha z^*\sigma dt. \end{aligned}$$

On the other hand, we obtain

$$\begin{aligned} d\kappa &= e^{\alpha z^*(\theta_t\omega)}dx + \alpha x e^{\alpha z^*(\theta_t\omega)}[-z^*dt + dW] \\ &= \frac{m(s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)})}{a + s_{in} + e^{-\alpha z^*(\theta_t\omega)}}\kappa dt - \bar{D}\kappa dt - \alpha z^*\kappa dt. \end{aligned}$$

Thus, we have the following random system

$$\frac{d\sigma}{dt} = -(\bar{D} + \alpha z^*)\sigma - \frac{m(s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)})}{a + s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)}}\kappa, \tag{1.9}$$

$$\frac{d\kappa}{dt} = -(\bar{D} + \alpha z^*)\kappa + \frac{m(s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)})}{a + s_{in} + \sigma e^{-\alpha z^*(\theta_t\omega)}}\kappa. \tag{1.10}$$

1.1.2 Random chemostat generates an RDS

Next we prove that the random chemostat given by (1.9)-(1.10) generates an RDS (see Appendix B for the definition). From now on, we will denote $\mathscr{X} := \{(x, y) \in \mathbb{R}^2 : x \in \mathbb{R}, y \geq 0\}$, the upper-half plane.

Theorem 1.1.1 *For any $\omega \in \Omega$ and any initial value $u_0 := (\sigma_0, \kappa_0) \in \mathscr{X}$, where $\sigma_0 := \sigma(0;0,\omega,u_0)$ and $\kappa_0 := \kappa(0;0,\omega,u_0)$, system* (1.9)-(1.10) *possesses a unique global solution $u(\cdot;0,\omega,u_0) := (\sigma(\cdot;0,\omega,u_0), \kappa(\cdot;0,\omega,u_0)) \in \mathscr{C}^1([0,+\infty),\mathscr{X})$ with $u(0;0,\omega,u_0) = u_0$. Moreover, the solution mapping generates an RDS $\varphi_u : \mathbb{R}^+ \times \Omega \times \mathscr{X} \to \mathscr{X}$ defined as*

$$\varphi_u(t,\omega)u_0 := u(t;0,\omega,u_0), \quad \text{for all } t \in \mathbb{R}^+,\ u_0 \in \mathscr{X},\ \omega \in \Omega,$$

the value at time t of the solution of system (1.9)-(1.10) *with initial value u_0 at time zero.*

Proof. Observe that we can rewrite one of the terms in the previous equations as

$$\frac{m(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa = \frac{m(s_{in}+\sigma e^{-\alpha z^*}+a-a)}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa = m\kappa - \frac{ma\kappa}{a+s_{in}+\sigma e^{-\alpha z^*}}$$

and therefore system (1.9)-(1.10) turns into

$$\frac{d\sigma}{dt} = -(\bar{D}+\alpha z^*)\sigma - m\kappa + \frac{ma}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa, \tag{1.11}$$

$$\frac{d\kappa}{dt} = -(\bar{D}+\alpha z^*)\kappa + m\kappa - \frac{ma}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa. \tag{1.12}$$

Denoting $u(\cdot;0,\omega,u_0) := (\sigma(\cdot;0,\omega,u_0), \kappa(\cdot;0,\omega,u_0))$, system (1.11)-(1.12) can be rewritten as

$$\frac{du}{dt} = L(\theta_t\omega)\ u + F(u,\theta_t\omega),$$

where

$$L(\theta_t\omega) = \begin{pmatrix} -(\bar{D}+\alpha z^*) & -m \\ 0 & -(\bar{D}+\alpha z^*)+m \end{pmatrix}$$

and $F : \mathscr{X} \times [0,+\infty) \longrightarrow \mathbb{R}^2$ is given by

$$F(\xi,\theta_t\omega) = \begin{pmatrix} \dfrac{ma}{a+s_{in}+\xi_1 e^{-\alpha z^*(\theta_t\omega)}}\xi_2 \\ \dfrac{-ma}{a+s_{in}+\xi_1 e^{-\alpha z^*(\theta_t\omega)}}\xi_2 \end{pmatrix},$$

where $\xi = (\xi_1,\xi_2) \in \mathscr{X}$.

Since $z^*(\theta_t\omega)$ is continuous, L generates an evolution system on $\mathbb{R}^2$. Moreover, we notice that

$$\frac{\partial}{\partial\xi_2}\left[\pm\frac{am}{a+s_{in}+\xi_1 e^{-\alpha z^*}}\xi_2\right] = \pm\frac{am}{a+s_{in}+\xi_1 e^{-\alpha z^*}}$$

and

$$\frac{\partial}{\partial \xi_1}\left[\pm\frac{am}{a+s_{in}+\xi_1 e^{-\alpha z^*}}\xi_2\right] = \mp\frac{ame^{-\alpha z^*}}{(a+s_{in}+\xi_1 e^{-\alpha z^*})^2}\xi_2,$$

thus $F(\cdot,\theta_t\omega)\in\mathscr{C}^1(\mathscr{X}\times[0,+\infty);\mathbb{R}^2)$ which implies that it is locally Lipschitz with respect to $(\xi_1,\xi_2)\in\mathscr{X}$. Therefore, thanks to classical results from the theory of ordinary differential equations, system (1.9)-(1.10) possesses a unique local solution. Now, we are going to prove that the unique local solution of system (1.9)-(1.10) is in fact a unique global one.

By defining $q(t):=\sigma(t)+\kappa(t)$ it is easy to check that q satisfies the differential equation

$$\frac{dq}{dt} = -(\bar{D}+\alpha z^*)q,$$

whose solution is given by the following expression

$$q(t;0,\omega,q_0) = q_0 e^{-\bar{D}t-\alpha\int_0^t z^*(\theta_s\omega)ds}. \tag{1.13}$$

The right side of (1.13) always tends to zero when t goes to infinity since $\bar{D}$ is positive, thus q is clearly bounded. Moreover, since

$$\left.\frac{d\sigma}{dt}\right|_{\sigma=0} = -\frac{ms_{in}}{a+s_{in}}\kappa < 0$$

we deduce that, if there exists some $t^*>0$ such that $\sigma(t^*)=0$, we will have $\sigma(t)<0$ for all $t>t^*$. Because of the previous reasoning, we will split our analysis into two different cases.

- **Case 1.** $\sigma(t)>0$ **for all** $t\geq 0$**:** in this case, from (1.9) we obtain

  $$\frac{d\sigma}{dt} \leq -(\bar{D}+\alpha z^*)\sigma$$

  whose solution satisfies

  $$\sigma(t;0,\omega,\sigma_0) \leq \sigma_0 e^{-\bar{D}t-\alpha\int_0^t z^*(\theta_s\omega)ds}.$$

  Since $\bar{D}$ is positive, we deduce that σ tends to zero when t goes to infinity, hence σ is bounded.

- **Case 2. There exists** $t^*>0$ **such that** $\sigma(t^*)=0$**:** in this case, we already know that $\sigma(t)<0$ for all $t>t^*$ and we claim that the following bound for σ holds true

  $$\sigma(t;0,\omega,\sigma_0) > -(a+s_{in})e^{\alpha z^*(\theta_t\omega)}. \tag{1.14}$$

To prove (1.14), we suppose that there exists $\bar{t} > t^* > 0$ such that

$$a + s_{in} + \sigma(\bar{t})e^{-\alpha z^*(\theta_{\bar{t}}\omega)} = 0,$$

then we can find some $\varepsilon(\omega) > 0$ small enough such that $\sigma(t)$ is strictly decreasing and

$$-(\bar{D} + \alpha z^*(\theta_t\omega)) - \frac{m(s_{in} + \sigma(t)e^{-\alpha z^*(\theta_t\omega)})}{a + s_{in} + \sigma(t)e^{-\alpha z^*(\theta_t\omega)}}\kappa(t) > 0 \tag{1.15}$$

holds for all $t \in [\bar{t} - \varepsilon(\omega), \bar{t})$. Hence, from (1.15) we have

$$\frac{d\sigma}{dt}(\bar{t} - \varepsilon(\omega)) > 0,$$

thus there exists some $\delta(\omega) > 0$ small enough such that $\sigma(t)$ is strictly increasing for all $t \in [\bar{t} - \varepsilon(\omega), \bar{t} - \varepsilon(\omega) + \delta(\omega))$, which clearly contradicts the uniqueness of solution. Hence, (1.14) holds true for all $t \in \mathbb{R}$ and we can also ensure that σ is bounded.

Since $\sigma + \kappa$ and σ are bounded in both cases, κ is also bounded. Hence, the unique local solution of system (1.9)-(1.10) is a unique global one. Moreover, the unique global solution of system (1.9)-(1.10) remains in $\mathscr{X}$ for every initial value in $\mathscr{X}$ since $\kappa \equiv 0$ solves the same system.

Finally, the mapping $\varphi_u : \mathbb{R}^+ \times \Omega \times \mathscr{X} \to \mathscr{X}$ given by

$$\varphi_u(t,\omega)u_0 \quad := \quad u(t;0,\omega,u_0), \quad \text{for all } t \geq 0,\ u_0 \in \mathscr{X},\ \omega \in \Omega,$$

defines an RDS. The proof of this statement follows trivially hence we omit it.

□

1.1.3 Random pullback attractor for the random system

Now, we study the existence of the random pullback attractor, describing explicitly its internal structure. For a short description concerning the main ingredientes involved in the theory of RDSs and the notation used in the sequel, we refer the reader to Appendix B. Particularly, we would like to emphasize that $\mathscr{E}(\mathscr{X})$ denotes the set of all tempered sets, $E(\omega)$, of $\mathscr{X}$ and we will take initial values in a certain tempered set $E(\theta_{-t}\omega)$.

Theorem 1.1.2 *For any $\varepsilon > 0$, there exists a tempered compact random absorbing set $B_\varepsilon(\omega) \in \mathscr{E}(\mathscr{X})$ for the RDS $\{\varphi_u(t,\omega)\}_{t\geq 0,\omega\in\Omega}$, that is, for any $E \in \mathscr{E}(\mathscr{X})$ and each $\omega \in \Omega$, there exists $T_E(\omega,\varepsilon) > 0$ such that*

$$\varphi_u(t,\theta_{-t}\omega)E(\theta_{-t}\omega) \subseteq B_\varepsilon(\omega), \qquad \textit{for all } t \geq T_E(\omega,\varepsilon).$$

Proof. Thanks to (1.13), we have

$$q(t;0,\theta_{-t}\omega,q_0) \quad = \quad q_0 e^{-\bar{D}t - \alpha\int_{-t}^0 z^*(\theta_s\omega)ds} \quad \overset{t\to+\infty}{\longrightarrow} \quad 0.$$

Stochastic disturbances on the input flow

Then, for any $\varepsilon > 0$ there exists $T_E(\omega, \varepsilon) > 0$ such that, for all $t \geq T_E(\omega, \varepsilon)$ and $u_0 \in E(\theta_{-t}\omega)$, we obtain

$$-\varepsilon \leq q(t; 0, \theta_{-t}\omega, q_0) \leq \varepsilon.$$

If we assume that $\sigma(t) \geq 0$ for all $t \geq 0$, which corresponds to the **Case 1** in the proof of Theorem 1.1.1, since $\kappa(t) \geq 0$ for all $t \geq 0$, we have that

$$B_\varepsilon^1(\omega) := \{(\sigma, \kappa) \in \mathscr{X} \, : \, \sigma \geq 0, \sigma + \kappa \leq \varepsilon\}$$

is a tempered compact random absorbing set in $\mathscr{X}$.

Otherwise, i.e., if there exists some $t^* > 0$ such that $\sigma(t^*) = 0$, which corresponds to the **Case 2** in the proof of Theorem 1.1.1, from (1.14), we can deduce that

$$\sigma(t; 0, \theta_{-t}\omega, u_0) > -(a + s_{in})e^{\alpha z^*(\omega)}.$$

Hence, we obtain that

$$B_\varepsilon^2(\omega) := \left\{(\sigma, \kappa) \in \mathscr{X} \, : \, -\varepsilon - (a + s_{in})e^{\alpha z^*(\omega)} \leq \sigma \leq 0, -\varepsilon \leq \sigma + \kappa \leq \varepsilon\right\}$$

is a tempered compact random absorbing set in $\mathscr{X}$.

In conclusion, defining

$$B_\varepsilon(\omega) = B_\varepsilon^1(\omega) \cup B_\varepsilon^2(\omega) = \left\{(\sigma, \kappa) \in \mathscr{X} \, : \, -\varepsilon \leq \sigma + \kappa \leq \varepsilon, \sigma \geq -(a + s_{in})e^{\alpha z^*(\omega)} - \varepsilon\right\},$$

we obtain (see Figure 1.1) that $B_\varepsilon(\omega)$ is a tempered compact random absorbing set in $\mathscr{X}$ for every $\varepsilon > 0$.

□

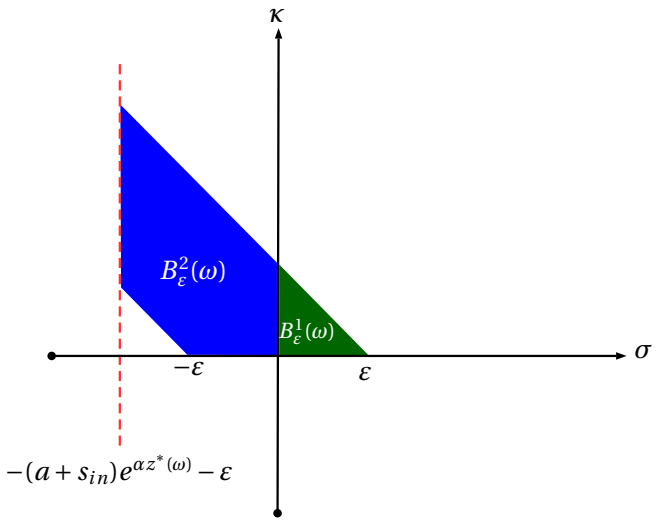


Figure 1.1: Absorbing set $B_\varepsilon(\omega) := B_\varepsilon^2(\omega) \cup B_\varepsilon^1(\omega)$

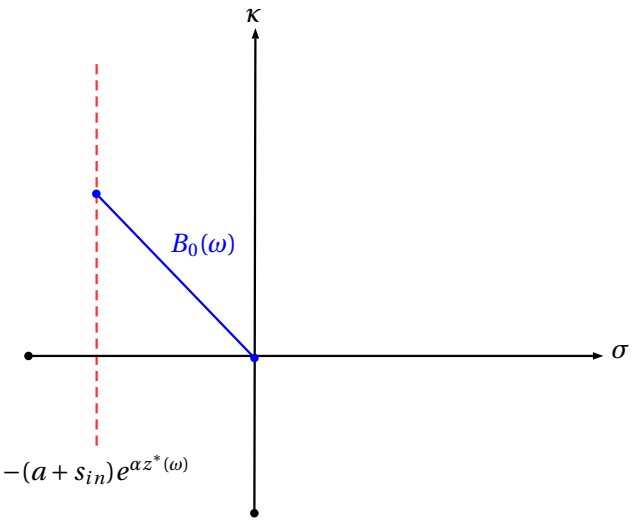


Figure 1.2: Absorbing set $B_0(\omega)$

Then, thanks to Proposition B.0.1 in Appendix B, it follows directly that system (1.9)-(1.10) possesses a unique random pullback attractor given by

$$\mathscr{A}(\omega) \subseteq B_\varepsilon(\omega), \qquad \text{for all } \varepsilon > 0,$$

thus

$$\mathscr{A}(\omega) \subseteq B_0(\omega),$$

where

$$B_0(\omega) := \left\{(\sigma,\kappa) \in \mathscr{X} \,:\, \sigma+\kappa = 0, \sigma \geq -(a+s_{in})e^{\alpha z^*(\omega)}\right\}$$

is a tempered compact random absorbing set (see Figure 1.2) in $\mathscr{X}$.

The following result provides information about the internal structure of the unique random pullback attractor.

Proposition 1.1.1 *The unique random pullback attractor of system* (1.9)-(1.10) *consists of a singleton component given by* $\mathscr{A}(\omega) = \{(0,0)\}$ *as long as*

$$\bar{D} > \mu(s_{in}) \tag{1.16}$$

holds true.

Proof. We would like to note that the result in this proposition follows trivially if σ remains always positive (**Case 1** in the proof of Theorem 1.1.1) since in that case both σ and κ are positive and $\sigma+\kappa$ tends to zero when t goes to infinity, thus the random pullback attractor is directly given by $\mathscr{A}(\omega) = \{(0,0)\}$.

Due to the previous reason, we only present the proof if there exists some $t^* > 0$ such that $\sigma(t^*) = 0$. In such a case, we know that $\sigma(t) < 0$ for all $t > t^*$ whence $s(t) < s_{in}$ for all $t > t^*$. Then, $\mu(s) \leq \mu(s_{in})$ for all $t > t^*$ since $\mu(s) = ms/(a+s)$ is an increasing function. Hence, from (1.10) we have

$$\frac{d\kappa}{dt} \;\leq\; -(\bar{D}+\alpha z^*)\kappa + \frac{ms_{in}}{a+s_{in}}\kappa,$$

which implies the following inequality

$$\kappa(t;t^*,\theta_{-t}\omega,\kappa(t^*)) \;\leq\; \kappa(t^*)e^{-\left(\bar{D}-\frac{ms_{in}}{a+s_{in}}\right)(t-t^*)-\alpha\int_{-t}^{t^*} z^*(\theta_s\omega)ds},$$

where the right-hand side tends to zero when t goes to infinity as long as (1.16) is fulfilled, therefore the unique random pullback attractor is given by $\mathscr{A}(\omega) = \{(0,0)\}$.

□

1.1.4 Random pullback attractor for the stochastic system

We have proved that the system (1.9)-(1.10) has a unique global solution $u(t;0,\omega,u_0)$ which remains in $\mathscr{X}$ for all $u_0 \in \mathscr{X}$ and generates the RDS $\{\varphi_u(t,\omega)\}_{t\geq 0,\omega\in\Omega}$.

Stochastic disturbances on the input flow

Now, we define a mapping

$$\mathscr{T} : \Omega \times \mathscr{X} \longrightarrow \mathscr{X}$$

as follows

$$\mathscr{T}(\omega, \zeta) = \mathscr{T}(\omega, (\zeta_1, \zeta_2)) = \begin{pmatrix} (\zeta_1 - s_{in}) e^{\alpha z^*(\omega)} \\ \zeta_2 e^{\alpha z^*(\omega)} \end{pmatrix}$$

whose inverse is given by

$$\mathscr{T}^{-1}(\omega, \zeta) = \begin{pmatrix} s_{in} + \zeta_1 e^{-\alpha z^*(\omega)} \\ \zeta_2 e^{-\alpha z^*(\omega)} \end{pmatrix}.$$

We know that $v(t) = (s(t), x(t))$ and $u(t) = (\sigma(t), \kappa(t))$ are related by (1.7)-(1.8). Since $\mathscr{T}$ is a homeomorphism, thanks to Lemma B.0.1 in Appendix B we obtain a conjugated RDS which is given by

$$\begin{aligned}
\varphi_v(t,\omega)v_0 &:= \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)\mathscr{T}(\omega, v_0)) \\
&= \mathscr{T}^{-1}\left(\theta_t\omega, \varphi_u(t,\omega)\begin{pmatrix} (s(0) - s_{in}) e^{\alpha z^*(\omega)} \\ x(0) e^{\alpha z^*(\omega)} \end{pmatrix}\right) \\
&= \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)u_0) \\
&= \mathscr{T}^{-1}(\theta_t\omega, u(t;0,\omega,u_0)) \\
&= \begin{pmatrix} s_{in} + \sigma(t) e^{-\alpha z^*(\theta_t\omega)} \\ \kappa(t) e^{-\alpha z^*(\theta_t\omega)} \end{pmatrix} \\
&= v(t;0,\omega,v_0)
\end{aligned}$$

which means that $\{\varphi_v(t,\omega)\}_{t\geq 0, \omega\in\Omega}$ is an RDS for our original stochastic system (1.5)-(1.6).

Consequently, φ_v has a unique random pullback attractor $\mathscr{A}^{\mathscr{T}}(\omega) = \mathscr{T}^{-1}\mathscr{A}(\omega)$ (see Lemma B.0.2 in Appendix B) which satisfies that $\mathscr{A}^{\mathscr{T}}(\omega) \subseteq B_0^{\mathscr{T}}(\omega)$, where

$$B_0^{\mathscr{T}}(\omega) := \{(s,x) \in \mathscr{X} \ : \ s + x = s_{in}, \ s \geq -a\}. \tag{1.17}$$

In addition, under (1.16), the unique random pullback attractor for (1.5)-(1.6) reduces to a singleton subset $\mathscr{A}^{\mathscr{T}}(\omega) = \{(s_{in}, 0)\}$, which means that the microorganisms become extinct.

We remark that it is not possible to provide conditions which ensure the persistence of the microbial biomass even though our numerical simulations will show that we can get it for many different values of the parameters involved in the system, as we will present in Section 1.1.5. Consequently, it is not possible to prove mathematically the persistence of the microbial biomass in our model. This drawback is owing to the fact that the standard Wiener process is a non-bounded noise, therefore the perturbed input flow $D + \alpha\dot{W}(t)$ could be occasionally large, either positive or negative. By taking into account the previous reason, it is not surprising that it is not possible to ensure the persistence of the species despite of obtaining it numerically when the realizations of the noise are not too large such that $D + \alpha\dot{W}(t)$ remains positive

for every time.

1.1.5 Numerical simulations and final comments

To support the results obtained in this chapter, in this section we will show some numerical simulations concerning the original stochastic chemostat model given by system (1.5)-(1.6).

First of all, we will present the numerical scheme to be used since it will be the same in the rest of the dissertation. We firstly consider the following abstract system of stochastic differential equations in Stratonovich sense

$$dX(t) = f(X(t))dt + g(X(t)) \circ dW(t), \quad X(0) = X_0, \tag{1.18}$$

where $X \in \mathbb{R}^d$, and $X_0 \in \mathbb{R}^d$ denotes the value of the unique global solution of the differential equation in (1.18) at time zero. In the sequel, $d = 3$ and $d = 2$ will correspond to the stochastic chemostat models with and without wall growth, respectively.

Now we define a partition $\Delta := \{0 = \tau_0 < \tau_1 < \cdots < \tau_N = T\}$ by splitting the time interval $[0, T] \subset \mathbb{R}$, $T > 0$, into N subintervals and setting $\delta t = T/N$ and $\tau_j = j\,\delta t$, for $j = 0, \ldots, N$. Our aim is to approximate $X(\tau_j) \approx X_j$ by using the Euler-Maruyama method (see [50] for more detailed information).

In this way we integrate the differential equation in (1.18) on $\tau_{j-1} \leq t \leq \tau_j$ for some arbitrary $j \in \{0, \ldots, N\}$ and we use the following approximations of both deterministic and stochastic integrals

$$\int_{\tau_{j-1}}^{\tau_j} f(X(s))ds \approx f(X_{j-1})\delta t$$

and

$$\int_{\tau_{j-1}}^{\tau_j} g(X(s))dW(s) \approx g(X_{j-1})\delta W_j,$$

where $\delta W_j := W(\tau_j) - W(\tau_{j-1}) \sim \mathcal{N}(0, \delta t)$ are independent normally distributed random variables.

Hence, we can already define the following numerical scheme given by

$$X_j = X_{j-1} + F(X_{j-1})\delta t + G(X_{j-1})\delta W_j$$

for every $j = 1, \ldots, N$.

Concerning our stochastic chemostat model, it can be then discretized as follows

$$\begin{aligned} s_j &= s_{j-1} + F_1(x_{j-1}, s_{j-1})\Delta t + G_1(x_{j-1}, s_{j-1})\,(W(\tau_j) - W(\tau_{j-1})), \\ x_j &= x_{j-1} + F_2(x_{j-1}, s_{j-1})\Delta t + G_2(x_{j-1}, s_{j-1})\,(W(\tau_j) - W(\tau_{j-1})), \end{aligned}$$

for every $j = 1, \ldots, N$, where $F_1,\ G_1,\ F_2,\ G_2 : \mathbb{R}^d \longrightarrow \mathbb{R}$ are functions given by

$$\begin{aligned} F_1(x_{j-1}, s_{j-1}) &= (s_{in} - s_{j-1})\bar{D} - \frac{m s_{j-1} x_{j-1}}{a + s_{j-1}}, \\ F_2(x_{j-1}, s_{j-1}) &= x_{j-1}\left(\frac{m s_{j-1}}{a + s_{j-1}} - \bar{D}\right), \\ G_1(x_{j-1}, s_{j-1}) &= \alpha(s_{in} - s_{j-1}), \\ G_2(x_{j-1}, s_{j-1}) &= \alpha x_{j-1}. \end{aligned}$$

Having reached this point, we present different numerical simulations to show the dynamics of our original stochastic chemostat model (1.5)-(1.6). Particularly, we display the phase plane (s, x) of the corresponding model. The blue dashed lines represent the solutions of the deterministic (i.e., with $\alpha = 0$) system (1.1)-(1.2) and the other ones are different realizations of the stochastic chemostat model (1.5)-(1.6). In addition, we set $s_{in} = 1$, $a = 0.6$, $m = 3$ and we consider $(s(0), x(0)) = (2.5, 5)$ as initial pair. We also present different cases where the value of the dilution rate and the amount of noise change in order to obtain different situations in which condition (1.16) is (or is not) fulfilled.

On the one hand, in Figure 1.3 we take $D = 3$ and we choose $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right). In both cases, it is easy to check that $\bar{D} = 1.5050$ (left), $\bar{D} = 1.6250$ (right) and $\mu(s_{in}) = 1.8750$, thus thanks to Proposition 1.1.1, we know that the microorganisms become extinct, as we show in the simulations.

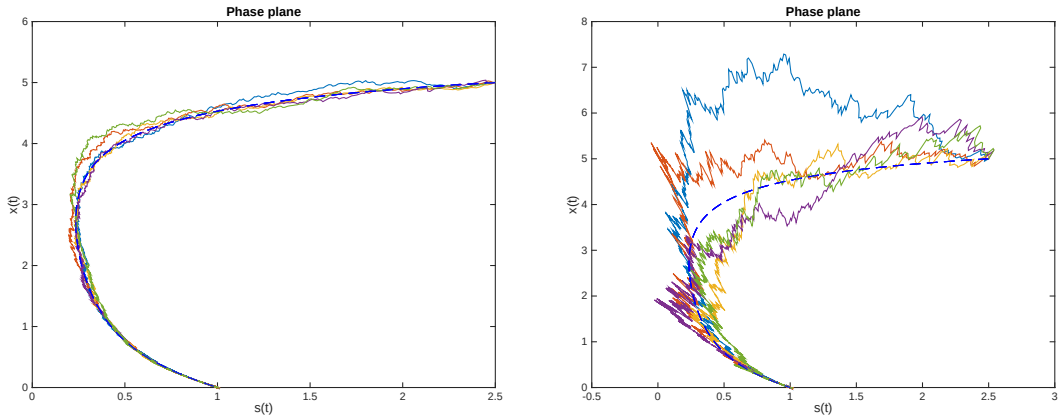


Figure 1.3: Extintion. $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right)

On the other hand, in Figure 1.4 we take $D = 3$ but, in this case, $\alpha = 1$ (left) and $\alpha = 1.5$ (right). Then, it follows that $\bar{D} = 2$ (left) and $\bar{D} = 2.6250$ (right) then, since $\mu(s_{in}) = 1.8750$ and thanks to Proposition 1.1.1, we also obtain the extinction of the species.

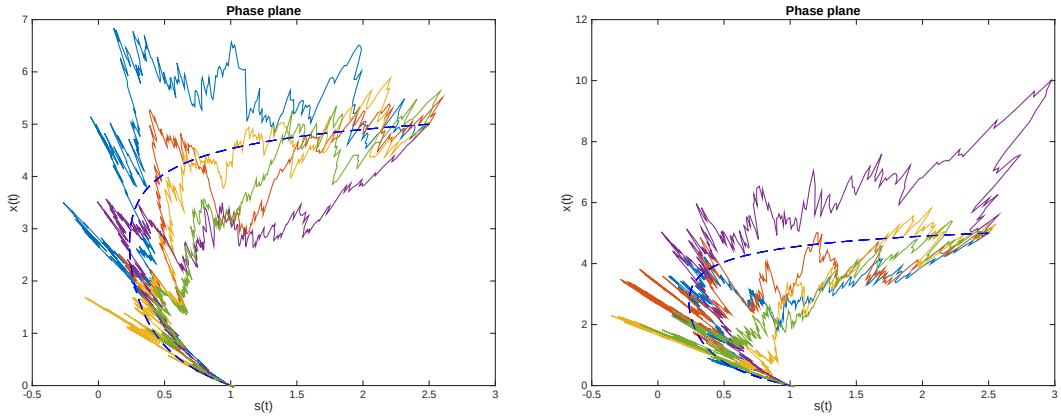


Figure 1.4: Extinction. $\alpha = 1$ (left) and $\alpha = 1.5$ (right)

Now, in Figure 1.5 we take $D = 1.5$ and we choose $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right). Then, we can check that $\bar{D} = 1.5050$ (left), $\bar{D} = 1.6250$ (right) and $\mu(s_{in}) = 1.8750$ thus, although it is not possible to ensure mathematically the persistence of the microbial biomass, we can get it for the previous values of the parameters, as it can be observed in the simulations.

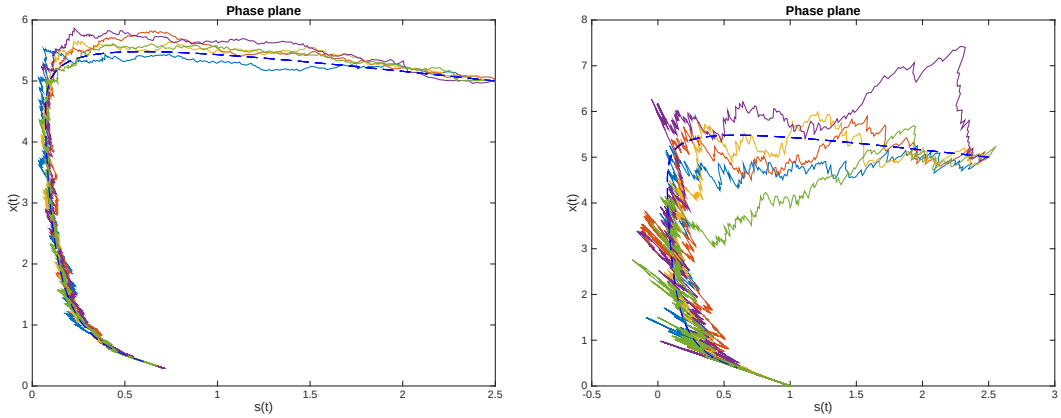


Figure 1.5: Persistence. $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right)

However, in Figure 1.6 we take $D = 1.5$, $\alpha = 1$ (left) and $\alpha = 1.5$ (right). Since condition (1.16) holds true, it is not surprising to obtain the extinction of the microorganisms.

Stochastic disturbances on the input flow

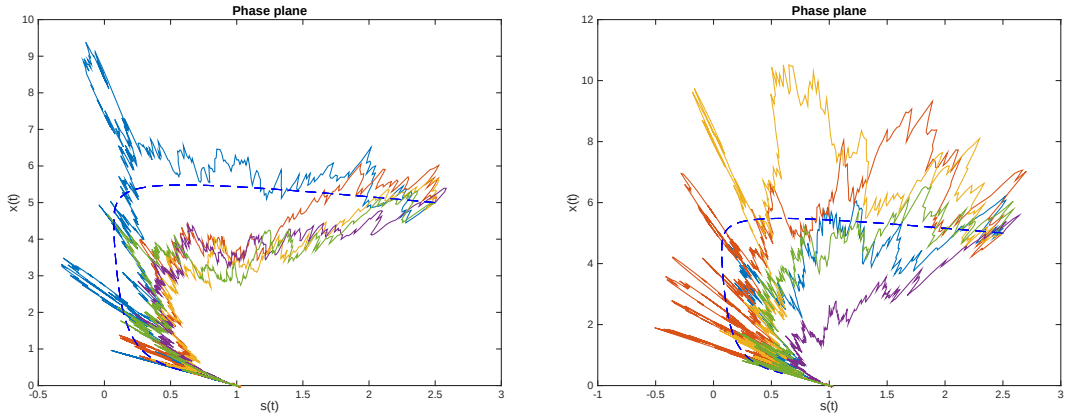


Figure 1.6: Extinction. $\alpha = 1$ (left) and $\alpha = 1.5$ (right)

Finally, in Figure 1.7 we take $D = 0.8$ and we choose $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right). It is easy to check that $\bar{D} = 0.8050$ (left), $\bar{D} = 0.9250$ (right) and $\mu(s_{in}) = 1.8750$, thus although it is not possible to guarantee mathematically the persistence of the species, since (1.16) is not fulfilled, we can obtain it in this case.

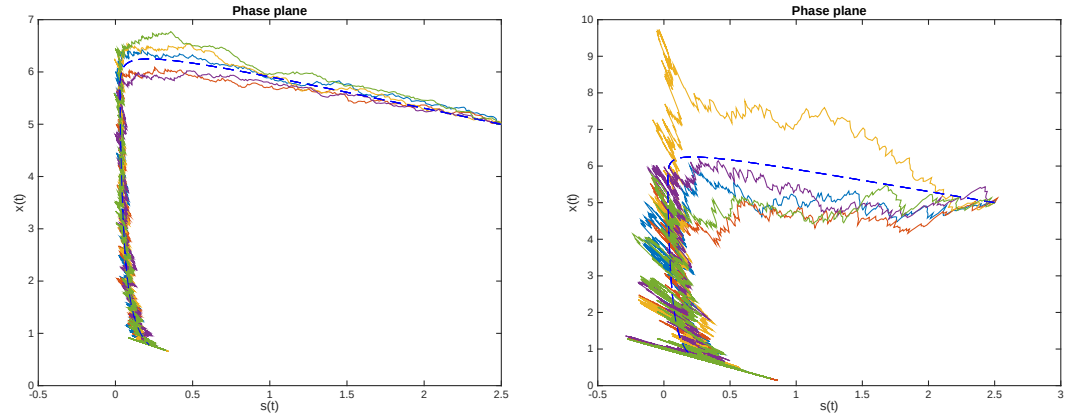


Figure 1.7: Persistence. $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right)

We would like to mention that the fact that the substrate s (or its corresponding state variable σ) may take negative values does not produce any mathematical inconsistence in our analysis, in other words, our mathematical analysis is accurate to handle the mathematical problem. However, from a biological point of view, this may reflect some troubles and suggests that either the fact of perturbing the dilution rate with an additive noise may not be a realistic situation, or that we should try to use a some kind of switching system to model our real chemostat in such a way that when the dilution may be negative we use a different equation to model the system. This will lead us to consider a different way to model the deterministic

chemostats in the following chapters by introducing a different kind of randomness or stochasticity in the input flow, as we will make in Chapter 2, or designing a different model for our problem, as it will be made in Chapters 3 and 4.

1.2 Stochastic chemostat model with wall growth

In this section we will analyze the chemostat model with wall growth (6)-(8) influenced by a standard Wiener process, in the same way than in Section 1.1. Our main goal now is to study the effects produced by a non-bounded noise on a chemostat model where the wall growth is also taken into account.

Let us recall the deterministic chemostat model with wall growth and Monod kinetics, which is given by the following differential system

$$\frac{ds}{dt} = D(s_{in}-s) - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + b\nu x_1, \tag{1.19}$$

$$\frac{dx_1}{dt} = -(\nu+D)x_1 + \frac{cs}{a+s}x_1 - r_1x_1 + r_2x_2, \tag{1.20}$$

$$\frac{dx_2}{dt} = -\nu x_2 + \frac{cs}{a+s}x_2 + r_1x_1 - r_2x_2, \tag{1.21}$$

where $s(t)$, $x_1(t)$ and $x_2(t)$ denote concentrations of the nutrient and the two different microorganisms, respectively; $b \in (0,1)$ describes the fraction of dead biomass which is recycled, $\nu > 0$ is the collective death rate coefficient, $r_1 > 0$ and $r_2 > 0$ represent the rates at which the species stick on to and shear off the walls of the culture vessel, respectively, and $0 < c \leq m$ is the growth rate coefficient of the consumer species.

Our aim now is to perturb the input flow by the standard Wiener process in the same way that in the previous section, i.e., we will replace the parameter D by $D + \alpha\dot{W}(t)$ in the deterministic chemostat model with wall growth (1.19)-(1.21), where $\alpha > 0$ represents the intensity of the noise and W denotes the white noise again, such that the following stochastic system understood in Itō sense is obtained

$$\begin{aligned}
ds &= \left[D(s_{in}-s) - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + b\nu x_1\right]dt + \alpha(s_{in}-s)dW(t),\\
dx_1 &= \left[-(\nu+D)x_1 + \frac{cs}{a+s}x_1 - r_1x_1 + r_2x_2\right]dt - \alpha x_1 dW(t),\\
dx_2 &= \left[-\nu x_2 + \frac{cs}{a+s}x_2 + r_1x_1 - r_2x_2\right]dt.
\end{aligned}$$

After making use of the well-known conversion between Itō and Stratonovich sense, we have the following stochastic system in Stratonovich sense

$$ds = \left[\bar{D}(s_{in}-s) - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + b\nu x_1\right]dt + \alpha(s_{in}-s)\circ dW(t), \tag{1.22}$$

Stochastic disturbances on the input flow

$$dx_1 = \left[-(\nu+\bar{D})x_1 + \frac{cs}{a+s}x_1 - r_1x_1 + r_2x_2\right]dt - \alpha x_1 \circ dW(t), \tag{1.23}$$

$$dx_2 = \left[-\nu x_2 + \frac{cs}{a+s}x_2 + r_1x_1 - r_2x_2\right]dt, \tag{1.24}$$

where $\bar{D} = D + \frac{\alpha^2}{2}$.

1.2.1 Stochastic chemostat becomes a random chemostat

In this section, we will analyze the stochastic chemostat model with wall growth (1.22)-(1.24) by performing a variable change which involves the Ornstein-Uhlenbeck process, similarly to the case already studied in the previous section. To this end, we firstly define the following state variables

$$\sigma(t) = (s(t) - s_{in})e^{\alpha z^*(\theta_t\omega)}, \tag{1.25}$$

$$\kappa_1(t) = x_1(t)e^{\alpha z^*(\theta_t\omega)}, \tag{1.26}$$

$$\kappa_2(t) = x_2(t), \tag{1.27}$$

where the last variable κ_2 remains as x_2 due to the fact that equation (1.24) is not affected by the stochastic perturbation. For the sake of simplicity, we will write again z^* instead of $z^*(\theta_t\omega)$ and $\sigma, \kappa_1, \kappa_2$ in place of $\sigma(t), \kappa_1(t), \kappa_2(t)$.

From (1.25)-(1.27), by differentiation, we obtain the following differential system satisfied by σ, κ_1 and κ_2, respectively,

$$\frac{d\sigma}{dt} = -(\bar{D}+\alpha z^*)\sigma - \frac{m(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa_1 - \frac{m(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa_2 e^{\alpha z^*} + b\nu\kappa_1, \tag{1.28}$$

$$\frac{d\kappa_1}{dt} = -(\nu+\bar{D}+\alpha z^*)\kappa_1 + \frac{c(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa_1 - r_1\kappa_1 + r_2\kappa_2 e^{\alpha z^*}, \tag{1.29}$$

$$\frac{d\kappa_2}{dt} = -\nu\kappa_2 + \frac{c(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa_2 + r_1\kappa_1 e^{-\alpha z^*} - r_2\kappa_2. \tag{1.30}$$

Now, we will perform another variable change to transform the random system (1.28)-(1.30) into another one where the total biomass and the proportion of one of the species play an important and helpful role. To this end, we define the new state variables

$$\kappa(t) = \kappa_1(t) + \kappa_2(t), \tag{1.31}$$

$$\xi(t) = \frac{\kappa_1(t)}{\kappa_1(t)+\kappa_2(t)}. \tag{1.32}$$

We also write in this case κ and ξ instead of $\kappa(t)$ and $\xi(t)$ in order to make the readability easier.

From (1.31)-(1.32), by differentiation, we have the following random system satisfied by σ, κ and ξ, respectively,

$$\frac{d\sigma}{dt} = -(\bar{D}+\alpha z^*)\sigma - \frac{m(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\xi\kappa - \frac{m(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}e^{\alpha z^*}\kappa(1-\xi)+b\nu\xi\kappa, \tag{1.33}$$

$$\frac{d\kappa}{dt} = -\nu\kappa-(\bar{D}+\alpha z^*)\kappa\xi+\frac{c(s_{in}+\sigma e^{-\alpha z^*})}{a+s_{in}+\sigma e^{-\alpha z^*}}\kappa+r_1\kappa\xi(e^{-\alpha z^*}-1)+r_2(1-\xi)\kappa(e^{\alpha z^*}-1), \tag{1.34}$$

$$\frac{d\xi}{dt} = -(\bar{D}+\alpha z^*)\xi(1-\xi)-r_1\xi+r_2e^{\alpha z^*}(1-\xi)-r_1(e^{-\alpha z^*}-1)\xi^2-r_2(e^{\alpha z^*}-1)\xi(1-\xi). \tag{1.35}$$

Instead of analyzing now the existence and uniqueness of global solution of our random system (1.33)-(1.35), we assume that there exists a unique global solution of the random chemostat model with wall growth which generates an RDS. Particularly, from (1.33), the random differential equations describing the dynamics of the substrate, we have the following equalities

$$\begin{aligned}\left.\frac{d\sigma}{dt}\right|_{\sigma=0} &= -\frac{ms_{in}}{a+s_{in}}\xi\kappa-\frac{ms_{in}}{a+s_{in}}e^{\alpha z^*}\kappa(1-\xi)+b\nu\xi\kappa,\\ &= -\frac{ms_{in}}{a+s_{in}}\kappa\left[\xi+e^{\alpha z^*}(1-\xi)\right]\\ &= \kappa\left[-\frac{ms_{in}}{a+s_{in}}\left(\xi+e^{\alpha z^*}(1-\xi)\right)+b\nu\xi\right].\end{aligned}$$

Thus, σ will remain positive as long as

$$\frac{ms_{in}}{a+s_{in}}\left(\xi(t)+e^{\alpha z^*(\theta_t\omega)}(1-\xi(t))\right)\leq b\nu\xi(t)$$

holds true for every $t\geq 0$ and any $\omega\in\Omega$ or, equivalently,

$$e^{\alpha z^*(\theta_t\omega)}\leq\left(\frac{b\nu\xi(t)(a+s_{in})}{ms_{in}}-\xi(t)\right)\frac{1}{1-\xi(t)}. \tag{1.36}$$

Thanks to (1.32), $0\leq\xi(t)\leq 1$ for every $t\geq 0$ since it is defined as the proportion of microorganisms in the liquid media. Hence, we have to distinguish the following situations:

- **Case 1.-** ξ **tends to one.** In this case, the quotient $1/(1-\xi(t))$ tends to infinity, thus (1.36) could be true. Nevertheless, it would mean that κ_2 (or its corresponding state variable x_2) tends to zero. Consequently, the microbial biomass sticked on the walls of the culture vessel would become extinct, then we would recover the stochastic chemostat model without taking into account the wall growth analyzed in Section 1.1.

- **Case 2.-** ξ **does not tend to one.** In this case, the right-hand side in (1.36) is bounded for every $t\geq 0$

and any $\omega \in \Omega$, whereas z^* could take arbitrary large values which means that (1.36) does not hold true and then σ can take negative values. In addition, it is not difficult to prove the following lower bound for σ, which is given by

$$\sigma(t) > -(a + s_{in})e^{\alpha z^*(\theta_t \omega)},$$

similarly to the proof made in Section 1.1.2, that implies

$$s(t) > -a.$$

As explained in Section 1.1, it is not realistic at all from the biological point of view and this is the main reason because we will not develop a deeper analysis of this kind of noise on the chemostat model with wall growth. Instead, we will consider the wall growth in the chemostat model when perturbing the system by means of other kinds of noise which are proved to be much more realistic and interesting from the biological point of view.

In those cases, we will present detailed proofs concerning the existence and uniqueness of global solution, the existence of an absorbing set which will help us to guarantee the existence and uniqueness of random pullback attractor and we will also ensure the persistence of both species in the *strong* sense (11). In addition, we will show several numerical simulations to support the results provided through the corresponding chapters.

1.2.2 Numerical simulations and final comments

Although we have not analyzed in much detail the chemostat model with wall growth due to the reasons explained before, we will show in this section some numerical simulations to remark the drawbacks found when using the Wiener process to perturb the input flow in the chemostat model with wall growth as well.

In this case, we also consider the same numerical scheme than the one used in Section 1.1.5. In each figure some different panels will be displayed. On the one hand, there is a big panel on the left, where we can see the phase plane showing the dynamics of the stochastic chemostat model with wall growth in Stratonovich sense (1.22)-(1.24). On the other hand, three different panels are stated on the right to describe the dynamics of the substrate and both species individually, depending on the time. We remark that these simulations are made in the pullback sense to see more easily the long-time behavior of the different state variables involved in the model. The blue dashed lines in the big panel represent the solutions of the deterministic system (1.19)-(1.21). In addition, we set $s_{in} = 1$, $a = 0.6$, $m = 3$, $r_1 = 0.6$, $r_2 = 0.4$ and we consider $(s(0), x_1(0), x_2(0)) = (5, 2.5, 2.5)$ as initial data. In this way, we present different cases where the value of the rest of the parameters change and the intensity of the noise increases or decreases, in order to show the effect of each one on the dynamics of our model.

On the one hand, in Figure 1.8 we take $D = 3$, $b = 2$, $\nu = 0.2$, $c = 1.5$ and we choose $\alpha = 0.5$. We can see that every state variable remains in the first octant in this case, i.e., they are all positive, however both species, the one in the medium or liquid media and also the one sticked on the walls, become extinct.

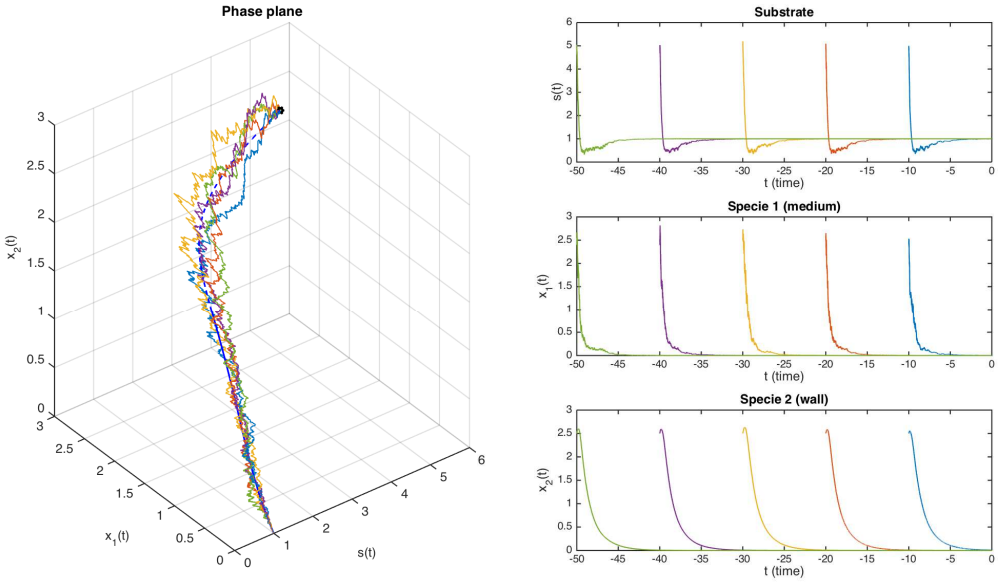


Figure 1.8: Extinction of both species. $\alpha = 0.5$

Similarly, in Figure 1.9 we take $D = 3$, $b = 2$, $\nu = 0.2$, $c = 1.5$ and we increase the intensity of the noise to $\alpha = 1.5$. In this case, both species become extinct and, moreover, the substrate reaches negative values for some times which is totally unrealistic from the biological point of view, as explained previously.

Stochastic disturbances on the input flow

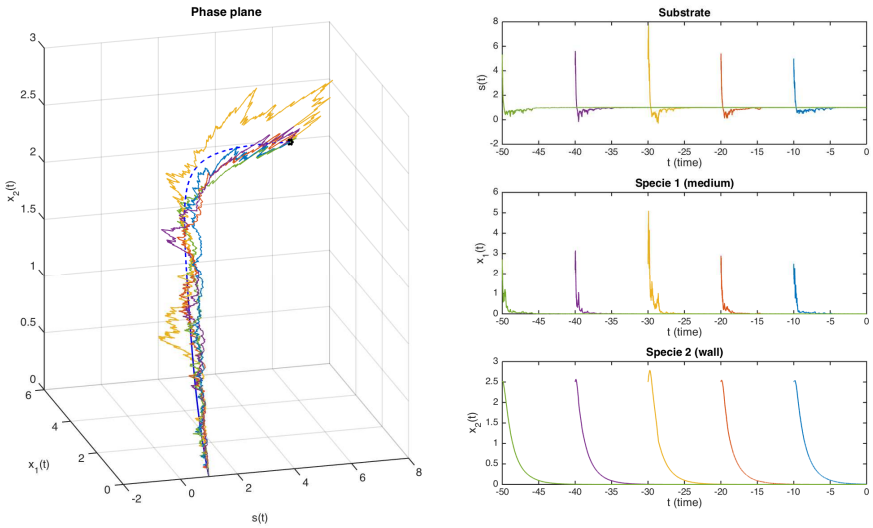


Figure 1.9: Extinction of both species. $\alpha = 1.5$

Now, in Figure 1.10 we take $D = 3$, $b = 0.5$, $\nu = 1.2$ and $\alpha = 0.5$. In this case, it is not difficult to notice that both species persist. Nevertheless, the dynamics of the substrate clearly cross the line $s = 0$ which is an important inconvenient.

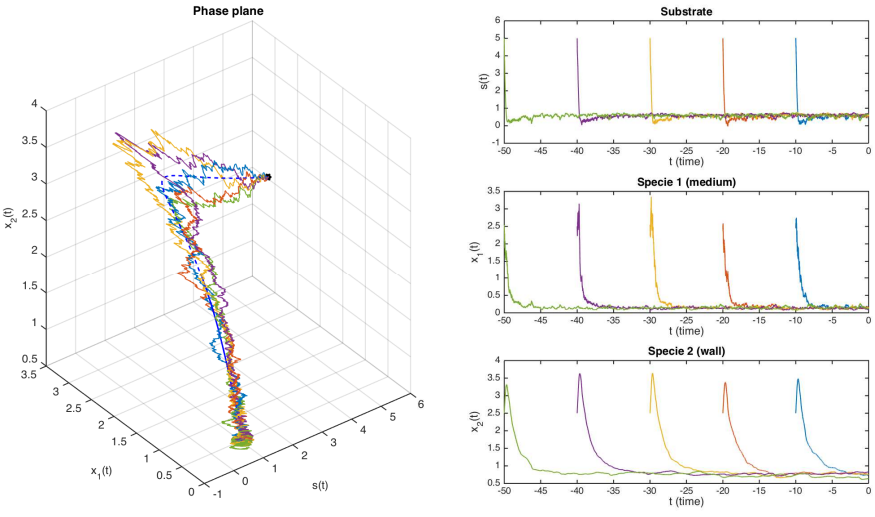


Figure 1.10: Persistence of both species. $\alpha = 0.5$

Finally, in Figure 1.11 we take $D = 3$, $b = 0.5$, $\nu = 1.2$ and $\alpha = 1.5$. In this case, the species which are sticked on the walls of the culture vessel persist whereas the ones in the liquid media become extinct. In addition, we also find some drawbacks since the substrate reaches negative values.

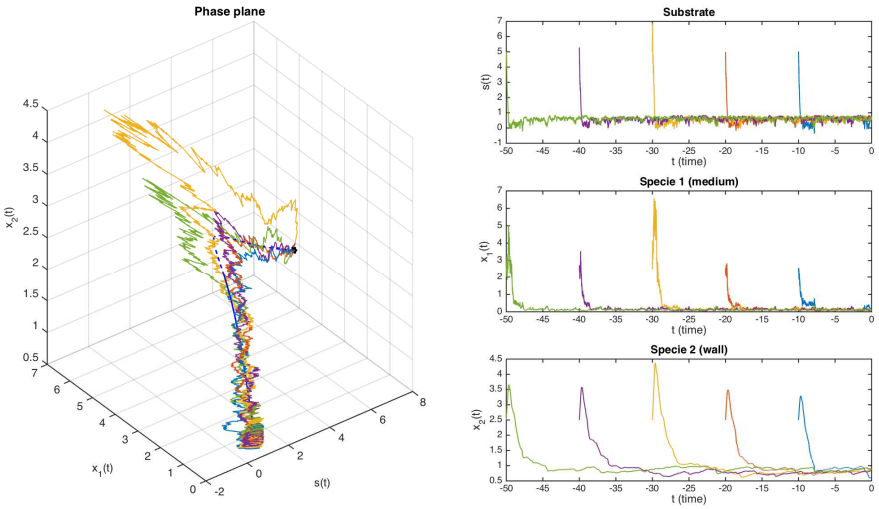


Figure 1.11: Persistence and extinction. $\alpha = 1.5$

CHAPTER 2

Modeling and analysis of random disturbances on the input flow in chemostat models

In this chapter, we will consider both chemostat models, with and without wall growth, where the input flow is perturbed by means of the Ornstein-Uhlenbeck process which is, differently to the standard Wiener process, a bounded noise. In this case, we will set up a new framework. Particularly, a parameter β will be introduced as drift in the Langevin equation that allows to bridge a gap between a pure Wiener process and no noise at all. This parameter, whose value is related to the amplitude of the deviations observed on the realizations, acts a a control in practice. In such a way, the resulting random differential system may not generate a random dynamical system, nevertheless this does not represent any inconvenient for the analysis of its long-time behavior, since it can be investigated for every fixed event ω. Thanks to this new approach, we will prove the existence and uniqueness of positive global solution of our models as well as the existence of both deterministic absorbing and attracting sets for the solutions of our system, in order to obtain detailed information regarding its asymptotic dynamics. However, the most interesting point is that such sets will be deterministic and will be obtained forwards in time, which is a relevant achievement respect to the case when dealing with random dynamical systems and pullback attractors. In addition, we will ensure the previous sets to be strictly positive, which means that the persistence of the species will be ensured. That is, needless to say, the main purpose of biologists. Finally, several numerical simulations will be presented to support the provided results. Apart from that, some comparisons between the way of perturbing the input flow in this chapter and Chapter 1 will be stated and some discussions and conclusions concerning the use of bounded noise to perturb the input flow in the chemostat models will be also provided.

The results and explanations concerning the contributions of this chapter can be found in [12, 60].

2.1 A new framework to deal with the Ornstein-Uhlenbeck process

In this first section, we set a new framework which will be highly useful and will consist in the key to ensure the persistence of the species under some *smallness* conditions on certain parameters involved in the chemostat model such as the dilution rate, the amplitude or intensity of the noise and also the collective death rate of the species in the model with wall growth. This new approach, in addition, will allow us to prove the existence of both absorbing and attracting sets forwards in time and, what is more interesting, independently on the noise.

At first, let us consider W being a two sided standard Wiener process. As explained in Appendix A, Kolmogorov's theorem ensures that W has a continuous version, that we will denote by ω, whose canonical interpretation is as follows: let $\Omega = \mathscr{C}_0(\mathbb{R}, \mathbb{R})$, the space of continuous functions that are zero at zero, $\mathscr{F}$ the Borel $\sigma-$algebra on Ω generated by the compact open topology (see [4] for details) and $\mathbb{P}$ the corresponding Wiener measure on $\mathscr{F}$. We consider now the Wiener shift flow given by

$$\theta_t\omega(\cdot) = \omega(\cdot + t) - \omega(t), \quad \text{for all } t \in \mathbb{R}.$$

Then, $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$ defines a metric dynamical system (see Appendix A for details).

Now, we introduce a new suitable Ornstein-Uhlenbeck process, as a generalization of the one defined in (A.1) in Appendix A, by considering some parameters on the drifts of the stochastic process which allow us to control the realizations of the noise in some sense. To this end, we present the following Ornstein-Uhlenbeck process on the metric dynamical system $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$, which is defined as the random variable given by

$$z^*_{\beta,\nu}(\theta_t\omega) = -\beta\nu \int_{-\infty}^{0} e^{\beta s}\theta_t\omega(s)ds, \quad \text{for all } t \in \mathbb{R},\ \omega \in \Omega,\ \beta > 0,\ \nu > 0, \tag{2.1}$$

which solves the following Langevin equation (see [4, 18, 19])

$$dz + \beta z dt = \nu d\omega(t), \quad \text{for all } t \in \mathbb{R}. \tag{2.2}$$

The Ornstein-Uhlenbeck process given by (2.1) is a stationary mean-reverting Gaussian stochastic process where $\beta > 0$ is the mean reversion constant that represents the strength with which the process is attracted by the mean or, in other words, how *strongly* our system reacts under some perturbation, and $\nu > 0$ is the volatility constant which represents the variation or the size of the noise independently of the amount of the noise $\alpha > 0$. In fact, the Ornstein-Uhlenbeck process can describe the position of some particle by taking into account the friction, which is the main difference with the standard Wiener process and makes our model to be a better approach to the real ones. In addition, the Ornstein-Uhlenbeck process can be understood as a kind of *generalization* of the standard Wiener process, which would correspond to take $\beta = 0$ and $\nu = 1$ in (2.1).

Random disturbances on the input flow

By taking into account the definition of both parameters β and ν involved in the Langevin equation (2.2), we highlight the following relevant observations concerning the effects caused by each of them on the evolution of the stochastic process.

• **Fixed $\beta > 0$.** Then, the volatility of the process is larger if we consider a larger ν. However, the evolution of the process is considerably smoother when we take a smaller value of ν. This is quite reasonable since ν decides the amount of noise introduced to dz, which measures the variation of the stochastic process, hence the process will be subjected to suffer much more changes when choosing a larger value of ν. We can easily observe this behavior in Figure 2.1 where we simulate two typical realizations of the perturbed dilution rate $D+\alpha z^*_{\beta,\nu}(\theta_t\omega)$ with $D = 2$, $\alpha = 0.8$, $\beta = 2$ and we consider $\nu = 0.1$ (blue) and $\nu = 0.5$ (orange).

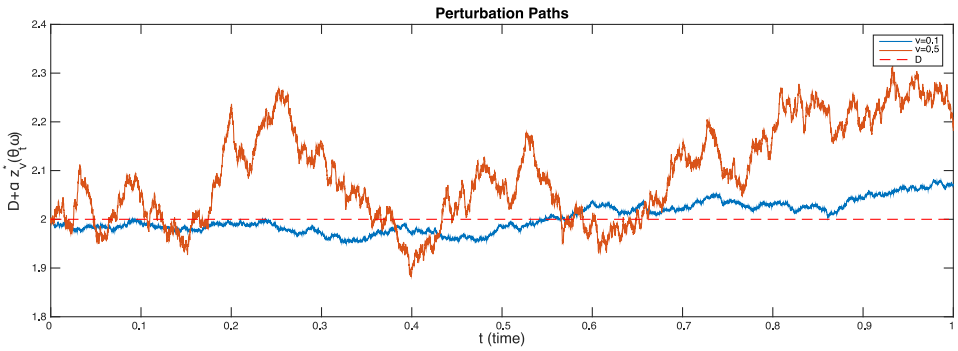


Figure 2.1: Realizations of the perturbed dilution rate with $D = 2$, $\alpha = 0.8$ and $\beta = 2$

• **Fixed $\nu > 0$.** Then, the process tends to go further away from the mean value if we consider a smaller value of β. However, the attraction of the mean increases when taking a larger β, which is absolutely logical since β has a huge influence on the drift of the Langevin equation (2.2). For instance, we can observe this behavior in Figure 2.2, where we simulate two realizations of the perturbed dilution rate $D + \alpha z^*_{\beta,\nu}(\theta_t\omega)$ with $D = 2$, $\alpha = 0.8$, $\nu = 0.5$ and we take $\beta = 2$ (blue) and $\beta = 10$ (orange).

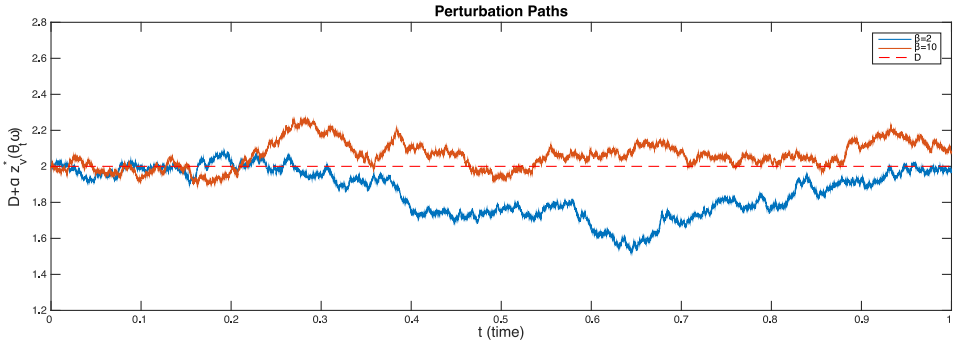


Figure 2.2: Realizations of the perturbed dilution rate with $D = 2$, $\alpha = 0.8$ and $\nu = 0.5$

We establish below an important result involving some ergodic properties held by the Ornstein-Uhlenbeck process (2.1) which will be used at several places in the sequel.

Proposition 2.1.1 *There exists a θ_t-invariant set $\widetilde{\Omega} \in \mathscr{F}$ of Ω of full $\mathbb{P}-$measure such that for $\omega \in \widetilde{\Omega}$ and $\beta, \nu > 0$, we have*

(i) the random variable $|z^*_{\beta,\nu}(\omega)|$ is tempered (see Definition B.0.3 in Appendix B).

(ii) the mapping

$$(t,\omega) \to z^*_{\beta,\nu}(\theta_t\omega) = -\beta\nu \int_{-\infty}^{0} e^{\beta s}(\theta_t\omega)(s)\,ds$$

is a stationary solution of (2.2) with continuous trajectories;

(iii) for any $\omega \in \tilde{\Omega}$ one has:

$$\begin{aligned}
\lim_{t\to\pm\infty} \frac{|z^*_{\beta,\nu}(\theta_t\omega)|}{t} &= 0;\\
\lim_{t\to\pm\infty} \frac{1}{t}\int_0^t z^*_{\beta,\nu}(\theta_s\omega)\,ds &= 0;\\
\lim_{t\to\pm\infty} \frac{1}{t}\int_0^t \left|z^*_{\beta,\nu}(\theta_s\omega)\right| ds &= \mathbb{E}\left[z^*_{\beta,\nu}\right] < \infty;
\end{aligned}$$

(iv) finally, for any $\omega \in \widetilde{\Omega}$,

$$\lim_{\beta\to+\infty} z^*_{\beta,\nu}(\theta_t\omega) = 0, \quad \text{for all } t \in \mathbb{R}.$$

Remark 2.1.1 *We note that the proof of (iv) can be found in [1] (see Lemma 4.1) and we refer the readers to [4, 18] for the proof of (i)-(iii).*

Random disturbances on the input flow

Then, we restrict the metric dynamical system previously introduced to $\widetilde{\Omega}$, such that we obtain a new metric dynamical system, see [14] for details. For simplicity, we denote again this new metric dynamical system by the old symbols, namely $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$.

Our aim in this section is to analyze both chemostat models with and without wall growth, where the input flow is perturbed by using the O-U process as explained before. To this end, let us first fix a strictly positive interval, namely $(b_1, b_2) \subset \mathbb{R}$, where $b_2 > b_1 > 0$. Thanks to the last item in Proposition 2.1.1, for each $\omega \in \Omega$, it is possible to choose $\beta \in \mathbb{R}$ large enough such that the corresponding realization of the perturbed input flow, $D + \alpha z^*_{\beta,\nu}(\theta_t\omega)$, remains inside the interval (b_1, b_2) for every $t \in \mathbb{R}$. Nevertheless, it is not possible to ensure, from a theoretical point of view, that there exists some $\beta \in \mathbb{R}$ such that almost all realizations of the perturbed input flow remains in (b_1, b_2), even though it seems to be true when making some numerical simulations. Because of this reason, we will analyze our random chemostat models, with and without wall growth, for every fixed $\omega \in \Omega$.

In the sequel, let us refer only to the chemostat model without wall growth in order to motivate our analysis, since the same arguments are valid for motivating the case with wall growth. As stated above, we know that it is possible to find $\beta_\omega \in \mathbb{R}$ such that $D + \alpha z^*_{\beta_\omega}(\theta_t\omega) \in (b_1, b_2)$ for every $t \in \mathbb{R}$, then we need to analyze the following random system

$$\frac{ds}{dt} = (s_{in} - s)\left[D + \alpha z^*_{\beta_\omega,\nu}(\theta_t\omega)\right] - \mu(s)x, \tag{2.3}$$

$$\frac{dx}{dt} = -\left[D + \alpha z^*_{\beta_\omega,\nu}(\theta_t\omega)\right]x + \mu(s)x. \tag{2.4}$$

We would like to remark that the choice of β depends on $\omega \in \Omega$, this is the reason to write β_ω in the previous system. Then, β_ω acts in practice as a control parameter. As a consequence, since $\beta_\omega \in \mathbb{R}$ depends on the event ω previously fixed, the solutions of system (2.3)-(2.4) may not generate a random dynamical system. Nevertheless, this does not represent any inconvenient for the analysis of the long-time behavior of the random differential system (2.3)-(2.4) since it can be investigated, as pointed out before, for every fixed event ω. Therefore, once fixed an event $\omega \in \Omega$, we have that β_ω is also a fixed real number, thus we will rewrite $\beta_\omega = \beta$, for the sake of clarity. The interesting fact is that the attracting sets for the solutions will not depend on ω, so we will obtain a non random set where all solutions for all realizations will approach to.

Throughout the rest of the section, we prove the existence and uniqueness of a global solution of the corresponding system (2.3)-(2.4) as well as the existence of a strictly positive forward attracting set for the solutions of system (2.3)-(2.4), under some condition involving the parameters of the model, whence we will be able to ensure that the microorganism concentration will be also asymptotically inside a strictly positive interval or, in other words, we will guarantee the persistence of the species.

As pointed out previously, the same arguments are used to motivate the analysis of the corresponding random chemostat model with wall growth, as we will see in Section 2.3.

Before starting with the analysis previously motivated, let us define the following constants

$$\underline{s} := \mu^{-1}(b_1) \qquad \text{and} \qquad \bar{s} := \mu^{-1}(b_2), \tag{2.5}$$

which will be essential henceforth. In addition, we recall that

$$\mu(s) = \frac{ms}{a+s}, \qquad \text{for all } s \geq 0,$$

denotes the consumption function of the species. In Figure 2.3 where we plot the mapping $s \mapsto \mu(s)$ and overlap a realization of the perturbed input flow as well, without taking into account the dependency of time.

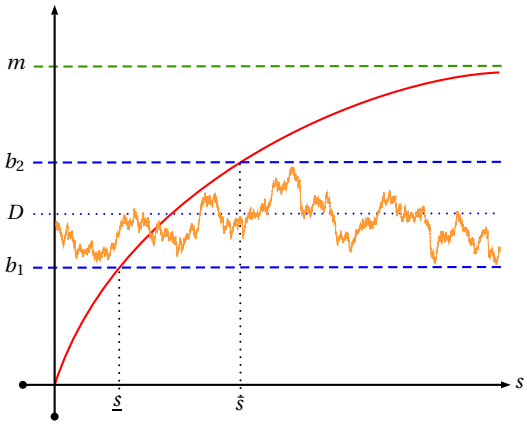


Figure 2.3: Realizations of the perturbed dilution rate, $\underline{s}$ and $\bar{s}$

Once presented this new framework, we will focus in the next sections on providing a careful analysis of both random chemostat models, with and without wall growth.

2.2 Random chemostat model

In this section we analyze the simplest chemostat model without wall growth where the input flow has been perturbed by using the Ornstein-Uhlenbeck process, which will lead us to deal with a random differential system in place of the stochastic one studied in Chapter 1.

Specifically, we are interested in analyzing the following random chemostat model

$$\frac{ds}{dt} = -\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right] s - \mu(s)x + s_{in}\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right], \tag{2.6}$$

$$\frac{dx}{dt} = -\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right] x + \mu(s)x. \tag{2.7}$$

Random disturbances on the input flow

Henceforth, $\omega \in \Omega$ is fixed and $\beta \in \mathbb{R}$ is also a parameter which has been fixed such that $D+\alpha z^*_{\beta,\nu}(\theta_t\omega) \in (b_1, b_2)$ for all $t \in \mathbb{R}$.

2.2.1 Existence and uniqueness of global solution

In this section, $\mathscr{X} = \{(x, y) \in \mathbb{R}^2 : x \geq 0,\ y \geq 0\}$ denotes the positive cone.

Theorem 2.2.1 *For any initial pair $v_0 := (s_0, x_0) \in \mathscr{X}$, system* (2.6)-(2.7) *possesses a unique global solution*

$$v(\cdot; 0, \omega, v_0) := (s(\cdot; 0, \omega, v_0), x(\cdot; 0, \omega, v_0)) \in \mathscr{C}^1([0, +\infty), \mathscr{X})$$

with $v(0; 0, \omega, v_0) = v_0$, where $s_0 := s(0; 0, \omega, v_0)$ and $x_0 := x(0; 0, \omega, v_0)$.

Proof. We set $v(\cdot; 0, \omega, v_0) := (s(\cdot; 0, \omega, v_0), x(\cdot; 0, \omega, v_0))$ such that system (2.6)-(2.7) can be rewritten as

$$\frac{dv}{dt} = L(\theta_t\omega)\ v + F(v, \theta_t\omega),$$

where

$$L(\theta_t\omega) \quad = \quad \begin{pmatrix} -(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) & -m \\ 0 & -(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) + m \end{pmatrix}$$

and $F : \mathscr{X} \times [0, +\infty) \longrightarrow \mathbb{R}^2$ is given by

$$F(\xi, \theta_t\omega) \quad = \quad \begin{pmatrix} \dfrac{ma}{a+\xi_1}\xi_2 + s_{in}D + \alpha s_{in} z^*_{\beta,\nu}(\theta_t\omega) \\ \dfrac{-ma}{a+\xi_1}\xi_2 \end{pmatrix},$$

where $\xi = (\xi_1, \xi_2) \in \mathscr{X}$.

Since $z^*_{\beta,\nu}(\theta_t\omega)$ is continuous, L generates an evolution system on $\mathbb{R}^2$. Moreover, we notice that $F(\cdot, \theta_t\omega) \in \mathscr{C}^1(\mathscr{X} \times [0, +\infty); \mathbb{R}^2)$ which implies that it is locally Lipschitz with respect to $(\xi_1, \xi_2) \in \mathscr{X}$. Therefore, system (2.6)-(2.7) possesses a unique local solution.

Now, we prove that the unique local solution of system (2.6)-(2.7) is defined for any forward time and is, then, a unique global one. To this end, we define the new state variable $q(t) := s(t) + x(t) - s_{in}$. Therefore, q satisfies the following differential equation

$$\frac{dq}{dt} = -\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right] q, \tag{2.8}$$

whose solution is given by

$$q(t; 0, \omega, q_0) = q_0 e^{-Dt - \alpha \int_0^t z^*_{\beta,\nu}(\theta_s\omega) ds}. \tag{2.9}$$

It is straightforward to check that q does not blow up at any finite time, thanks to the positiveness of the dilution rate and the ergodic properties satisfied by the O-U process (see Proposition 2.2.1, (iii)), what is more, q is bounded. In addition, after solving (2.7) we have the following upper bound for the x-equation

$$x(t;0,\omega,x_0) \leq x_0 e^{-(D-m)t-\alpha\int_0^t z^*_{\beta,\nu}(\theta_s\omega)ds},$$

since $\mu(s) \leq m$ for any $s \geq 0$.

In conclusion, x is also bounded by an expression which does not blow up at any finite time. Therefore, s does not blow up either and we can conclude that the chemostat model (2.6)-(2.7) possesses a unique global solution.

Moreover, since $x \equiv 0$ solves (2.7) and every realization of our noise remains in a strictly positive interval, we conclude that

$$\left.\frac{ds}{dt}\right|_{s=0} = \left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right] s_{in} > 0,$$

whence we can ensure the unique solution of system (2.6)-(2.7) to be in the positive cone $\mathscr{X}$ for every initial value $v_0 \in \mathscr{X}$.

□

2.2.2 Existence of a deterministic attracting set

Now, we are interested in proving the existence of an attracting set. From now on, $F \subset \mathscr{X}$ denotes a bounded set in the positive cone.

Theorem 2.2.2 *For any $\varepsilon > 0$, there exists a deterministic compact absorbing set $B_\varepsilon \subset \mathscr{X}$ for the solutions of our system* (2.6)-(2.7)*, i.e., there exists $T_F(\omega,\varepsilon) > 0$ such that for every given initial pair $v_0 \in F$, the solution corresponding to v_0 remains inside B_ε for all $t \geq T_F(\omega,\varepsilon)$.*

Proof. Consider again $q(t) = s(t) + x(t) - s_{in}$. Then, thanks to (2.9), we obtain

$$\lim_{t\to+\infty} q(t;0,\omega,q_0) = 0. \tag{2.10}$$

Thus, given $v_0 \in F$ and any $\varepsilon > 0$, there exists $T_F(\omega,\varepsilon) > 0$ such that

$$-\varepsilon \leq q(t;0,\omega,q_0) \leq \varepsilon$$

for every $t \geq T_F(\omega,\varepsilon)$.

Then,

$$B_\varepsilon := \{(s,x) \in \mathscr{X} \,:\, s_{in} - \varepsilon \leq s + x \leq s_{in} + \varepsilon\} \tag{2.11}$$

Random disturbances on the input flow

is a compact absorbing set in $\mathscr{X}$.

□

Therefore, thanks to Theorem 2.2.2, we have that

$$B_0 := \{(s,x) \in \mathscr{X} \,:\, s + x = s_{in}\} \tag{2.12}$$

is a deterministic attracting set for the solutions of our system (2.6)-(2.7) in forward sense, i.e.,

$$\lim_{t\to+\infty} \sup_{v_0\in F} \inf_{b_0\in B_0} |v(t;0,\omega,v_0) - b_0| = 0$$

holds true.

2.2.3 Internal structure of the deterministic attracting set

In this section, we analyze the internal structure of the deterministic attracting set B_0, given by (2.12). To this end, we develop a deeper analysis of both equations of the nutrient and microorganism concentration separately and we also take into account the asymptotic behavior of the total mass $s + x$.

Proposition 2.2.1 *Assume that the following condition*

$$D > \mu(s_{in}) \tag{2.13}$$

holds. Then, the corresponding deterministic attracting set for the solutions of the chemostat model (2.6)-(2.7) *is reduced to a singleton component which is given by* $\widehat{B}_0 = \{(s_{in}, 0)\}$.

Proof. We know that B_ε, which is given by (2.11), defines a compact absorbing set for the solutions of our system for every $\varepsilon > 0$. Then, there exists $T_F(\omega,\varepsilon) > 0$ such that for every given initial pair $v_0 \in F$, $s(t) \le s_{in}+\varepsilon$ for all $t \ge T_F(\omega,\varepsilon)$, whence we can deduce that $\mu(s(t)) \le \mu(s_{in}+\varepsilon)$ since $\mu(\cdot)$ is an increasing function. Therefore, from (2.7) we obtain

$$\frac{dx}{dt} \le -\left[D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right] x + \mu(s_{in}+\varepsilon)x,$$

whose solution satisfies

$$x(t;0,\omega,x_0) \le x_0 e^{-(D-\mu(s_{in}+\varepsilon))t - \alpha\int_0^t z^*_{\beta,\nu}(\theta_s\omega)ds}.$$

In addition, by assuming that condition (2.13) holds true, we know that there exists $\varepsilon_0 > 0$ such that $D > \mu(s_{in}+\varepsilon)$ for every $\varepsilon \in (0,\varepsilon_0)$. Thus, we can easily deduce that x tends to zero when t goes to infinity as long as (2.13) is satisfied.

Therefore, the attracting set for the solutions of the chemostat model (2.6)-(2.7) consists of a singleton component, which is given by $\widehat{B}_0 = \{(s_{in}, 0)\}$.

□

Remark 2.2.1 *We would like to highlight that Proposition 2.2.1 can be easily proved by assuming $D > m$. Nevertheless, assumption* (2.13) *is sharper than $D > m$ even though it requires a bit more of technicalities.*

The next result proves that it is possible to ensure the persistence of the microorganisms under some condition involving the parameters of the model.

Theorem 2.2.3 *Assume that*

$$\bar{s} < s_{in} \tag{2.14}$$

holds true, where $\bar{s}$ is defined as in (2.5)*. Then, for any $\varepsilon > 0$, there exists a deterministic compact absorbing set $\widehat{B}_\varepsilon \subset \mathscr{X}$, which is strictly contained in the positive cone $\mathscr{X}$, for the solutions of our chemostat model* (2.6)-(2.7)*.*

Proof. We recall that $q(t) = s(t) + x(t) - s_{in}$ satisfies the differential equation (2.8). Hence, from (2.10) we have that, for any $\varepsilon > 0$, there exists $T_F(\omega, \varepsilon) > 0$ such that for every given initial pair $v_0 \in F$, we obtain

$$-\varepsilon \leq q(t; 0, \omega, q_0) \leq \varepsilon \tag{2.15}$$

for every $t \geq T_F(\omega, \varepsilon)$.

Now, we analyze the differential equation for the substrate independently of the dynamics of system (2.6)-(2.7) since it will help us to guarantee the existence of a compact absorbing set for the substrate equation, which will be totally contained in the positive cone $\mathscr{X}$. Then, from (2.6), as $q(t) = s(t) + x(t) - s_{in}$, we have the following differential equation satisfied by the substrate

$$\begin{aligned} \frac{ds(t; 0, \omega, s_0)}{dt} &= (s_{in} - s(t; 0, \omega, s_0))(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(s(t; 0, \omega, s_0))q(t; 0, \omega, q_0) \\ &\quad -\mu(s(t; 0, \omega, s_0))(s_{in} - s(t; 0, \omega, s_0)). \end{aligned}$$

Hence, from (2.15) we can obtain the following bounds for the $s-$equation

$$\begin{aligned} \frac{ds(t; 0, \omega, s_0)}{dt} &\leq (s_{in} - s(t; 0, \omega, s_0))(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(s(t; 0, \omega, s_0))(s_{in} - s(t; 0, \omega, s_0)) \\ &\quad +\varepsilon m \end{aligned} \tag{2.16}$$

and

$$\begin{aligned} \frac{ds(t; 0, \omega, s_0)}{dt} &\geq (s_{in} - s(t; 0, \omega, s_0))(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(s(t; 0, \omega, s_0))(s_{in} - s(t; 0, \omega, s_0)) \\ &\quad -\varepsilon m, \end{aligned} \tag{2.17}$$

for every $v_0 \in F, \varepsilon > 0$ and for all $t \geq T_F(\omega, \varepsilon)$, where we recall that $\mu(s) < m$ for any $s > 0$.

We study now both differential inequalities (2.16) and (2.17) when $s = \underline{s}$ and $s = \bar{s}$, respectively, where $\underline{s}$ and $\bar{s}$ are defined as in (2.5). On the one hand, thanks to (2.14), we have

$$\begin{aligned} \left.\frac{ds(t;0,\omega,s_0)}{dt}\right|_{s=\bar{s}} &\leq (s_{in}-\bar{s})(D+\alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(\bar{s})(s_{in}-\bar{s}) + \varepsilon m \\ &\leq (s_{in}-\bar{s})\pi_- + \varepsilon m, \end{aligned}$$

for every $v_0 \in F, \varepsilon > 0$ and for all $t \geq T_F(\omega, \varepsilon)$, where $\pi_- := \sup_{t\geq 0} \pi_-(t)$ and $\pi_-(t) = (D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(\bar{s})$.

In this case, as long as we take $\varepsilon \in (0, -(s_{in}-\bar{s})\pi_-/m)$, we have $(s_{in}-\bar{s})\pi_- + \varepsilon m < 0$, and

$$\left.\frac{ds(t;0,\omega,s_0)}{dt}\right|_{s=\bar{s}} < 0. \tag{2.18}$$

On the other hand, from (2.14) we deduce that $s_{in} > \underline{s}$. Then, we similarly have

$$\begin{aligned} \left.\frac{ds(t;0,\omega,s_0)}{dt}\right|_{s=\underline{s}} &\geq (s_{in}-\underline{s})(D+\alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(\underline{s})(s_{in}-\underline{s}) - \varepsilon m \\ &\geq (s_{in}-\underline{s})\pi^+ - \varepsilon m, \end{aligned}$$

for every $v_0 \in F, \varepsilon > 0$ and for all $t \geq T_F(\omega, \varepsilon)$, where $\pi^+ := \inf_{t\geq 0} \pi^+(t)$ and $\pi^+(t) = (D + \alpha z^*_{\beta,\nu}(\theta_t\omega)) - \mu(\underline{s})$.

Now, it is enough to consider $\varepsilon \in (0, (s_{in}-\underline{s})\pi^+/m)$ in order to have $(s_{in}-\underline{s})\pi^+ - \varepsilon m > 0$. Thus,

$$\left.\frac{ds(t;0,\omega,s_0)}{dt}\right|_{s=\underline{s}} > 0. \tag{2.19}$$

From (2.18) and (2.19) we obtain a frame for the s variable:

$$\underline{s} < s(t;0,\omega,s_0) < \bar{s}$$

for every given $\varepsilon \in (0, \min\{(s_{in}-\bar{s})\pi^+/m, -(s_{in}-\bar{s})\pi_-/m\})$ and for all $t \geq T_F(\omega, \varepsilon)$, which means that the interval $(\underline{s}, \bar{s})$ is a deterministic absorbing set for equation (2.6) in forward sense.

In the sequel, we are able to guarantee the persistence of the microorganisms by proving that there also exists another deterministic absorbing set in forward sense, associated to the equation describing the dynamics of the microbial biomass, which is also totally contained in the positive cone $\mathscr{X}$.

As a consequence of the previous reasoning, we obtain the following inequalities

$$-\bar{s} + s_{in} - \varepsilon < x(t; 0, \omega, x_0) < -\underline{s} + s_{in} + \varepsilon,$$

for every given $\varepsilon \in (0, \min\{(s_{in} - \bar{s})\pi^+ / m, -(s_{in} - \bar{s})\pi_- / m\})$ and for all $t \geq T_F(\omega, \varepsilon)$.

Thanks to the previous study, we can deduce that the following deterministic set

$$\widehat{B}_\varepsilon = \{(s, x) \in \mathscr{X} \,:\, s_{in} - \varepsilon \leq s + x \leq s_{in} + \varepsilon,\ \underline{s} \leq s \leq \bar{s},\ s_{in} - \bar{s} - \varepsilon \leq x \leq s_{in} - \underline{s} + \varepsilon\}$$

defines a compact absorbing set for the solutions of our chemostat model (2.6)-(2.7) in forward sense.

□

Hence, we obtain that

$$\widehat{B}_0 = \{(s, x) \in \mathscr{X} \,:\, s + x = s_{in},\ \underline{s} \leq s \leq \bar{s},\ s_{in} - \bar{s} \leq x \leq s_{in} - \underline{s}\} \tag{2.20}$$

is a strictly positive deterministic compact attracting set for the solutions of (2.6)-(2.7) in forward sense (see Figure 2.4).

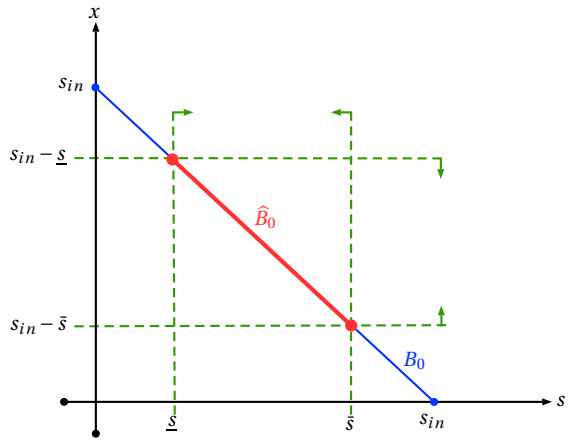


Figure 2.4: Attracting set $\widehat{B}_0$

We notice that, as long as condition (2.14) holds true, we obtain a new deterministic attracting set $\widehat{B}_0$ which is clearly smaller than the initial one B_0. Thus, we can ensure the persistence of the microbial biomass. What is more, the corresponding deterministic attracting set is obtained forwards in time, which makes itself even more interesting.

From Proposition 2.2.1, Theorem 2.2.3 and taking into account the arguments used in the corresponding proofs, it is possible to analyze all the cases involving both conditions (2.13) and (2.14) which are presented in Table 2.1 as a summary concerning the internal structure of the attracting set $\widehat{B}_0$, given by (2.20).

	$s_{in} > \bar{s}$	$s_{in} = \bar{s}$	$s_{in} < \bar{s}$
$D > \mu(s_{in})$	Not possible	Not possible	**Extinction (Proposition 2.2.1)** $\widehat{B}_0 = \{(s_{in}, 0)\}$ (washout equilibrium)
$D = \mu(s_{in})$	**Persistence (Theorem 2.2.3)** $s + x = s_{in}, \quad \underline{s} \leq s \leq \bar{s}$ $s_{in} - \bar{s} \leq x \leq s_{in} - \underline{s}$	Not possible to obtain (2.18). We can prove $\underline{s} \leq s \leq s_{in}, \quad 0 \leq x \leq s_{in} - \underline{s}$	Not possible to obtain (2.18). We can prove $\underline{s} \leq s \leq s_{in}, \quad 0 \leq x \leq s_{in} - \underline{s}$
$D < \mu(s_{in})$	Not possible	Not possible	Not possible to obtain (2.18). We can prove $\underline{s} \leq s \leq s_{in}, \quad 0 \leq x \leq s_{in} - \underline{s}$

Table 2.1: Internal structure of the deterministic attracting set $\widehat{B}_0$

In order to provide a complete description of the asymptotic behavior of the chemostat model with random input flow, we explain Table 2.1 in more detail. Firstly, it is easy to check that some cases are not compatible (it is enough to make a simple draw to notice it). In addition, thanks to Proposition 2.2.1 and Theorem 2.2.3, we know that the biomass becomes extinct as long as (2.13) holds true and we deduce persistence if (2.14) is fulfilled. However, there are more cases which can be analyzed. On the one hand, if $D = \mu(s_{in})$ and $s_{in} = \bar{s}$ hold true, we can check that it is possible to redo the proof of Theorem 2.2.3 but, in this case, (2.18) becomes an equality implying that the attracting set, $\widehat{B}_0$, is given by

$$\widehat{B}_0 = \{(s, x) \in \mathscr{X} \,:\, s + x = s_{in},\ \underline{s} \leq s \leq s_{in},\ 0 \leq x \leq s_{in} - \underline{s}\}. \tag{2.21}$$

On the other hand, as long as $s_{in} < \bar{s}$ and $D \leq \mu(s_{in})$ are fulfilled, we can also redo the proof of Theorem 2.2.3 but, in this case, we cannot obtain (2.18). Thus, the attracting set, $\widehat{B}_0$, is also given by (2.21).

From the previous analysis, it is worth mentioning that, differently to the deterministic case, where the washout equilibrium $(s_{in}, 0)$ is attractive if $D = \mu(s_{in})$ holds true (whence we obtain the extinction of the microbial biomass), see e.g. [49, 70], it is possible to deduce a relevant improvement when considering random disturbances on the input flow as in this section since, although it is not possible to guarantee the persistence of the microorganisms in the *strong* sense (11), we are able to ensure that the corresponding attracting set has several points (in fact, all of them except the washout) inside the positive cone.

2.2.4 Numerical simulations and final comments

In this section we would like to show some numerical simulations concerning the random chemostat model (2.6)-(2.7) in order to support the results proved throughout this section.

We remark that we use again the Euler-Maruyama method (see [50] for more detailed information) to define the numerical scheme necessary to obtain the numerical simulations, see Section 1.1.5 in Chapter 1 or [9,10,13].

In every simulation, the dashed lines represent the solution of the deterministic systems, i.e., the behavior of the stochastic/random system after taking $\alpha = 0$, whereas the continuous lines correspond to different realizations of the solution of the corresponding stochastic/random system.

Now, we show some simulations concerning the random chemostat model previously studied in Section 2.2. In each of the following figures three panels are displayed: the left one shows the phase plane and the general dynamics of the random chemostat model; the two panels on the right-hand side help us to see two important zones in the phase plane. These places are said to be important due to the fact that some notable changes can be observe in the dynamics of the system around these points.

In Figure 2.5 we set $D = 2, s_{in} = 4, a = 0.6, m = 5, \alpha = 0.5, \beta = 1, \nu = 0.7$ and initial values $s_0 = 2, x_0 = 5$ for the nutrient and the microorganisms, respectively. In this case (2.14) holds true and this is the reason why we can observe the persistence of the species. We can also see how the realizations are approaching to the line $s + x = s_{in}$, as proved in (2.12) and (2.20).

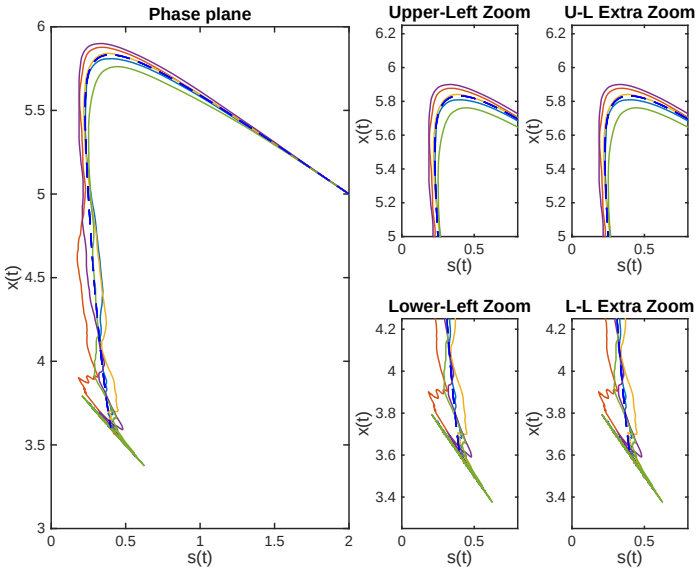


Figure 2.5: Persistence of the species in the random chemostat model

Random disturbances on the input flow

In the next two figures, we change the intensity of the noise and the parameters involved in the definition of the Ornstein-Uhlenbeck process. We will just specify those parameters to be changed in order not to be redundant. For instance, in Figure 2.6 we increase the intensity of the noise to $\alpha = 1$, the mean reversion constant to $\beta = 5$ and we slightly decrease the volatility constant to $\nu = 0.2$. In this case we can easily notice that the dynamics tends to the line $s + x = s_{in}$, as previously proved.

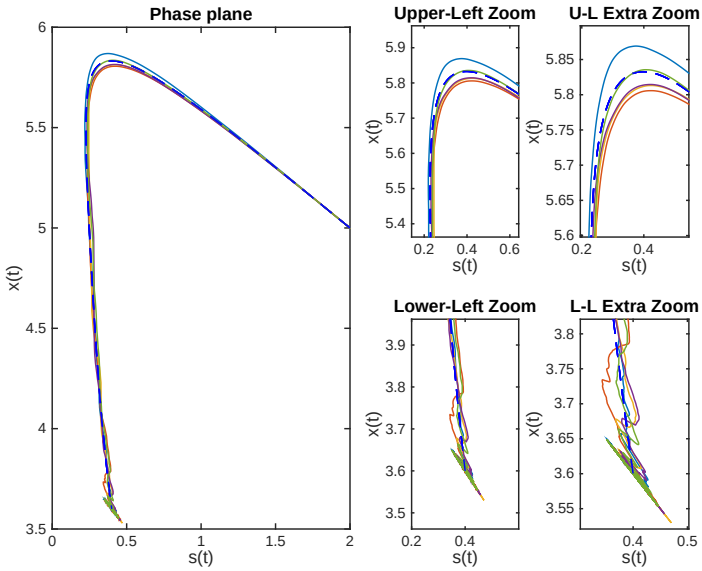


Figure 2.6: Persistence of the species in the random chemostat model (ii)

Furthermore, in Figure 2.7 we take $\alpha = 4$ and the rest of parameters are not changed respect to the last ones. We can also see the dynamics approaching to $x + s = s_{in}$ even though the quantity of noise is considerably large. In fact, by taking into account the model perturbed by using the white noise, as made in Chapter 1, we can check the high differences between both ways of modeling the disturbances on the input flow since here we can consider large values as $\alpha = 4$ whereas much smaller values, such as $\alpha = 1$ or even $\alpha = 0.5$, made some state variables take negative values in the case of considering the standard Wiener process. It is basically due to the fact that, in this case where we use the Ornstein-Uhlenbeck process, the parameter β plays an essential role in the sense that the intensity of the noise can be increased in exchange for increasing β.

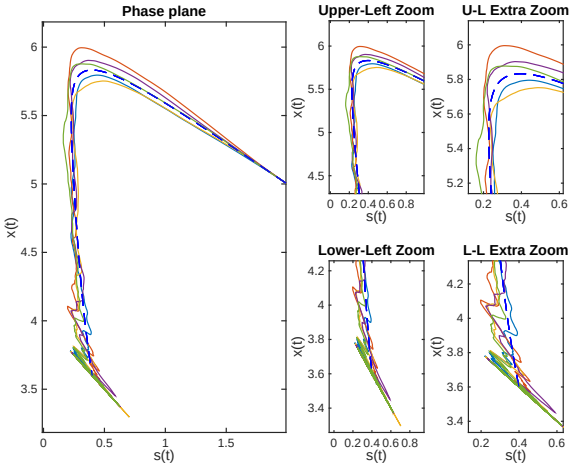


Figure 2.7: Persistence of the species in the random chemostat model (iii)

In Figure 2.8 we take $D = 3.5$, $s_{in} = 2$, $a = 0.8$, $m = 0.5$, $\alpha = 0.5$, $\beta = 1$, $\nu = 0.7$ and initial values $s_0 = 2.5$, $x_0 = 5$ for the nutrient and the microorganisms, respectively. Then we can see that the microorganisms extinguish, what is not surprising due to the fact that condition (2.13) is fulfilled. We can also see here how the realizations are approaching the line $s + x = s_{in}$, as proved in (2.12).

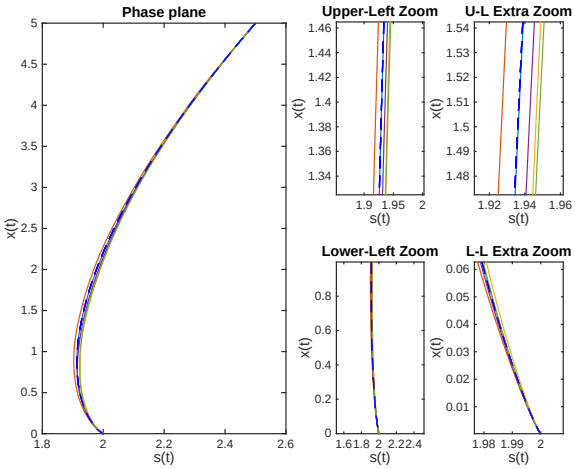


Figure 2.8: Extinction of the species in the random chemostat model

As made before, we only specify the parameters to be changed respect to the last ones considered. For example, in Figure 2.9 we increase the intensity of the noise and the mean reversion constant to $\alpha = 1$ and

$\beta = 5$, respectively. In addition, we slightly decrease the volatility constant to $\nu = 0.2$. In this case, it is straightforward to notice that, since (2.13) is true, the dynamics tend to $(s_{in}, 0)$, as proved in Proposition 2.2.1.

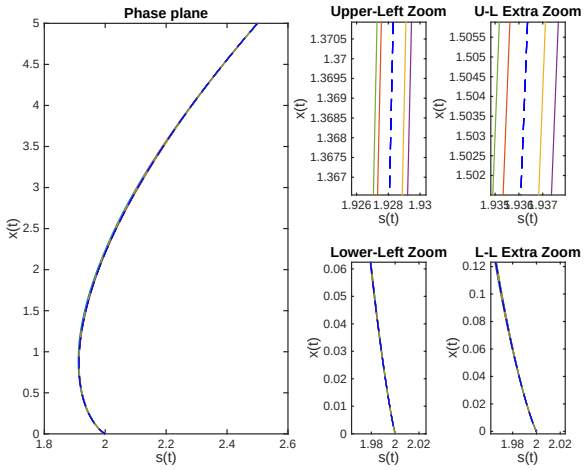


Figure 2.9: Extinction of the species in the random chemostat model (ii)

On the other hand, we change in Figure 2.10 the intensity of the noise to $\alpha = 4$ and we observe the same behavior, even though the quantity of noise is considerably large respect to the rest of the cases when perturbing the input flow by using the Ornstein-Uhlenbeck process and, what is more interesting, respect to the case when using the standard Brownian motion, as in Chapter 1.

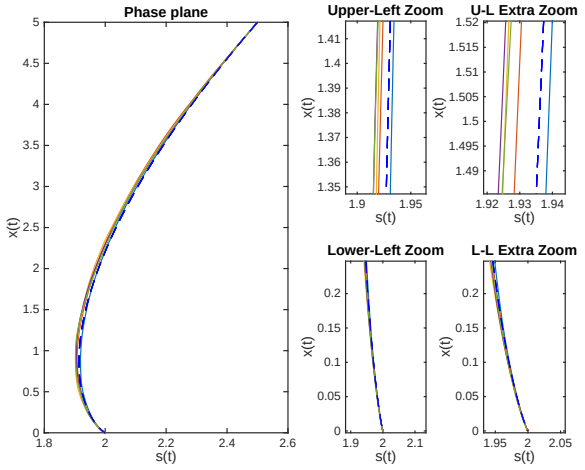


Figure 2.10: Extinction of the species in the random chemostat model (iii)

Next we present two figures where we overlap a typical realization of the solution of system (1.5)-(1.6) and another one of the solution of system (2.6)-(2.7) such that we can notice much more easily the differences between the simulations concerning the different ways of modeling randomness and stochasticity on the input flow. In each figure we display a big panel where the general dynamics can be seen and four smaller panels which correspond to two different zooms of two interesting places of the realizations, specifically the dynamics around $(s,x) = (2,2)$ and $(s,x) = (2,0)$ in Figure 2.11 and the dynamics about $(s,x) = (0.2,5.5)$ and $(s,x) = (0.4,3.75)$ in Figure 2.12.

In Figure 2.11 we plot a typical realization when perturbing the dilution rate with the standard Wiener process (orange) and two different ones when perturbing with the Ornstein-Uhlenbeck process for different values of the mean reversion constant $\beta = 2$ (red) and $\beta = 0.5$ (green). In this case, we take $s_{in} = 2$, $D = 3.5$, $a = 0.8$, $m = 0.5$, $\alpha = 0.8$, $\sigma = 0.8$, $x_0 = 5$ and $s_0 = 2.5$. We can easily observe that (2.13) and (1.16) are both fulfilled then the microorganisms become extinct, as we already proved in Sections 1.1.3 (see Proposition (1.1.1)) in Chapter 1 and 2.2.3 (see Proposition (2.2.1)) in Chapter 2.

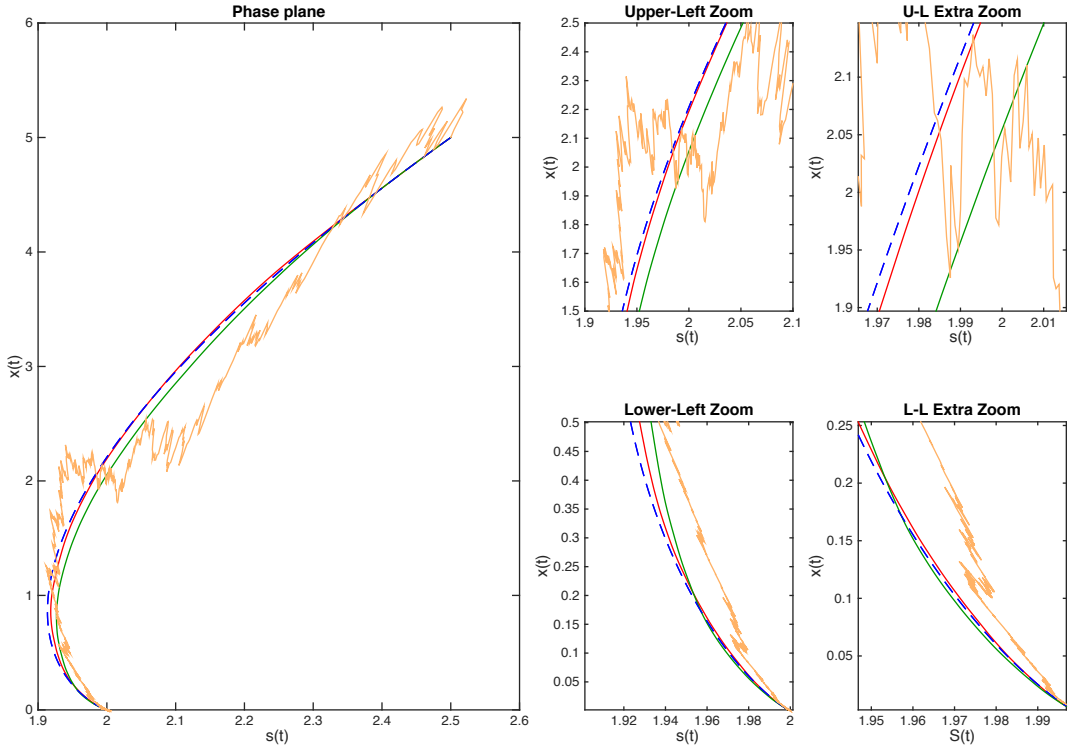


Figure 2.11: Comparison in case of extinction

Eventually, in Figure 2.12 we plot again a typical realization when perturbing the dilution rate with the

standard Wiener process (orange) and two different ones when perturbing by using the Ornstein-Uhlenbeck process for $\beta = 2$ (red) and $\beta = 0.5$ (green), but now we take $s_{in} = 4$, $D = 2$, $a = 0.6$, $m = 5$, $\alpha = 0.15$, $\sigma = 0.8$, $x_0 = 5$ and $s_0 = 2$. In this case (1.16) does not hold true, thus it is not possible to ensure the persistence of the species (in the chemostat model perturbed by using the standard Wiener process) although numerically it can be obtained for the previous values of the parameters. In addition, $D < \mu(s_{in})$ and $\bar{s} < s_{in}$ hold true, then we can ensure the persistence of the microbial biomass when perturbing the chemostat model by means of the Ornstein-Uhlenbeck process. Moreover, we can observe that every realization is approaching to the line $s + x = s_{in}$, as proved in Section 1.1.4 (see (1.17)) in Chapter 1 and Section 2.2.3 (see (2.20)) in Chapter 2.

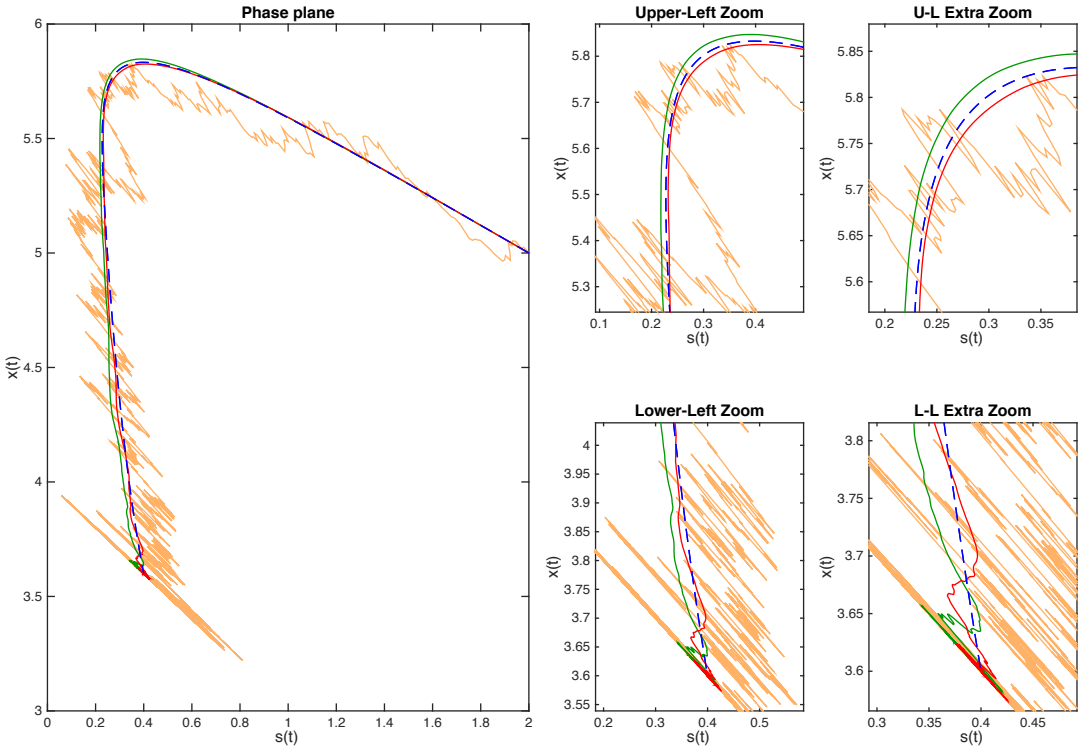


Figure 2.12: Comparison in case of persistence

In conclusion, we can observe that the Ornstein-Uhlenbeck process gives us a useful and interesting tool when modeling stochasticity and randomness since it allows us to set up mathematical models which guarantee the positiveness of the variable and therefore it better suits to represent reality. Moreover, the absorbing and attracting sets provided in the mathematical results are deterministic and forwards in time. This new framework could also allow us to revisit the persistence of species under input disturbances, for instance, in case of taking also into account the wall growth, as we will develop in Section 2.3.

2.3 Random chemostat model with wall growth

In this section, we are interested in analyzing the chemostat model with wall growth (6)-(8) where the input flow is perturbed by means of the Ornstein-Uhlenbeck process, similarly to Section 2.2.

2.3.1 Existence and uniqueness of global solution

We are interested in analyzing the following random differential system with wall growth and Monod kinetics

$$\frac{ds}{dt} = \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)(s_{in} - s) - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + b\nu x_1, \tag{2.22}$$

$$\frac{dx_1}{dt} = -\left(\nu + D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)x_1 + \frac{cs}{a+s}x_1 - r_1x_1 + r_2x_2, \tag{2.23}$$

$$\frac{dx_2}{dt} = -\nu x_2 + \frac{cs}{a+s}x_2 + r_1x_1 - r_2x_2, \tag{2.24}$$

where $z^*_{\beta,\nu}(\theta_t\omega)$ denotes, as in Section 2.2, the new Ornstein-Uhlenbeck process defined in (2.1). Henceforth, we consider $\omega \in \Omega$ to be fixed and, then, $\beta \in \mathbb{R}$ is also a fixed parameter such that $D + \alpha z^*_{\beta,\nu}(\theta_t\omega) \in (b_1, b_2)$ for every $t \in \mathbb{R}$.

In this section, $\mathcal{X} = \{(x, y, z) \in \mathbb{R}^3 : x \geq 0, y \geq 0, z \geq 0\}$ will denote the positive cone in the three-dimensional space.

Firstly, we will state a result concerning the existence and uniqueness of global solution of the chemostat model with wall growth (2.22)-(2.24).

Theorem 2.3.1 *For any initial triple $v_0 := (s_0, x_{10}, x_{20}) \in \mathcal{X}$, system* (2.22)-(2.24) *possesses a unique global solution*

$$v(\cdot; 0, \omega, v_0) := (s(\cdot; 0, \omega, v_0), x_1(\cdot; 0, \omega, v_0), x_2(\cdot; 0, \omega, v_0)) \in \mathcal{C}^1([0, +\infty), \mathcal{X})$$

with $v(0; 0, \omega, v_0) = v_0$, where $s_0 := s(0; 0, \omega, v_0)$, $x_{10} := x_1(0; 0, \omega, v_0)$ and $x_{20} := x_2(0; 0, \omega, v_0)$.

Proof. Let us recall that the random system (2.22)-(2.24) can be rewritten as

$$\frac{dv}{dt} = L(\theta_t\omega)\ v + F(v, \theta_t\omega),$$

where

$$L(\theta_t\omega) = \begin{pmatrix} -\left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) & -m + b\nu & -m \\ 0 & -\left(\nu + D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) - r_1 + c & r_2 \\ 0 & r_1 & -\nu + c - r_2 \end{pmatrix}$$

Random disturbances on the input flow

and $F : \mathscr{X} \times [0, +\infty) \longrightarrow \mathbb{R}^3$ is given by

$$F(\eta, \theta_t\omega) = \begin{pmatrix} \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} + \dfrac{ma}{a+\eta_1}\eta_2 + \dfrac{ma}{a+\eta_1}\eta_3 \\ -\dfrac{ca}{a+\eta_1}\eta_2 \\ -\dfrac{ca}{a+\eta_1}\eta_3 \end{pmatrix},$$

where $\eta = (\eta_1, \eta_2, \eta_3) \in \mathscr{X}$.

Since $z^*_{\beta,\nu}(\theta_t\omega)$ is continuous, L generates an evolution system on $\mathbb{R}^3$. Moreover, we notice that $F(\cdot, \theta_t\omega)$ $\in \mathscr{C}^1\left(\mathscr{X} \times [0, +\infty); \mathbb{R}^3\right)$ which implies that it is locally Lipschitz with respect to $(\eta_1, \eta_2, \eta_3) \in \mathscr{X}$. Therefore, system (2.22)-(2.24) possesses a unique local solution.

Now, we prove that the unique local solution of system (2.22)-(2.24) is defined for any forward time and is, then, a unique global one. To this end, we define the new state variable $p(t) = s(t) + \frac{m}{c}(x_1(t) + x_2(t))$ and take into account that $D + \alpha z^*_{\beta,\nu}(\theta_t\omega) > b_1 > 0$ for every $t \in \mathbb{R}$, $c \leq m$ and $b \leq 1$. Thus we have that p satisfies the next random differential inequalities

$$\begin{aligned} \frac{dp}{dt} &= \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} - \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s - \left[\frac{m}{c}\left(\nu + D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) - b\nu\right] x_1 - \frac{m}{c}\nu x_2 \\ &\leq \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} - b_1 s - \frac{m}{c} b_1 x_1 - \frac{m}{c}\nu x_2 \\ &\leq \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} - \vartheta\left[s + \frac{m}{c}x_1 + \frac{m}{c}x_2\right] \\ &= \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} - \vartheta p(t), \end{aligned}$$

or, in other words, p verifies the following random differential equation

$$\frac{dp}{dt} \leq \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} - \vartheta p(t), \tag{2.25}$$

where $\vartheta := \min\{b_1, \nu\} > 0$.

By solving (2.25), we have

$$p(t; 0, \omega, p_0) \leq p_0 e^{-\vartheta t} + s_{in} \int_0^t \left(D + \alpha z^*_{\beta,\nu}(\theta_s\omega)\right) e^{-\vartheta(t-s)}\, ds. \tag{2.26}$$

We remark that the integrand in (2.26) converges to zero for every $t \geq s \geq 0$ when t goes to infinity, but not the integral. Moreover, the integral has subexponential growth.

Therefore, p does not blow up at any finite time, thus s, x_1 and x_2 do not blow up at any finite time either. Hence, the solution of system (2.22)-(2.24) is defined for any forward time, whence we can straightforwardly deduce that the unique local solution of our system (2.22)-(2.24) is, in fact, a unique global one.

Now, we are going to prove that the previous unique global solution remains in the positive cone $\mathscr{X}$ for every initial value $v_0 \in \mathscr{X}$. To this end, we firstly consider $x_1 \geq 0$ and $x_2 \geq 0$ and we evaluate the random differential equation for the substrate when $s = 0$ such that we have

$$\left.\frac{ds}{dt}\right|_{s=0} = \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} + b\nu x_1 > 0$$

due to the fact that the perturbed input flow is always positive. Moreover, for every $s \geq 0$ and $x_2 \geq 0$, from the equation of the microorganisms in the liquid media, we have

$$\left.\frac{dx_1}{dt}\right|_{x_1=0} = r_2 x_2 \geq 0$$

and, for every $s \geq 0$ and $x_1 \geq 0$, from the species which are sticked on the walls of the culture vessel, we have

$$\left.\frac{dx_2}{dt}\right|_{x_2=0} = r_1 x_1 \geq 0.$$

Thus, the unique global solution $v(t;0,\omega,v_0)$ of our random system (2.22)-(2.24) remains in the positive cone $\mathscr{X}$ for every initial value $v_0 \in \mathscr{X}$.

□

2.3.2 Existence of a deterministic attracting set

In this section, we study the existence of a deterministic compact absorbing set as well as the existence of a deterministic attracting set, both of them forwards in time, for the solutions of our random chemostat model with wall growth (2.22)-(2.24).

Theorem 2.3.2 *For any given $\varepsilon > 0$, there exists a deterministic compact absorbing set $B_\varepsilon \subset \mathscr{X}$ for the solutions of system* (2.22)-(2.24)*, i.e., there exists $T_F(\omega,\varepsilon) > 0$ such that for every given initial pair $v_0 \in F$, the solution corresponding to v_0 remains inside B_ε for all $t \geq T_F(\omega,\varepsilon)$.*

Proof. Consider again the state variable $p(t) = s(t) + \frac{m}{c}(x_1(t) + x_2(t))$. Then, from (2.26) we obtain

$$\begin{aligned} p(t;0,\omega,p_0) &\leq p_0 e^{-\vartheta t} + s_{in}\int_0^t \left(D + \alpha z^*_{\beta,\nu}(\theta_s\omega)\right) e^{-\vartheta(t-s)}\,ds \\ &\leq p_0 e^{-\vartheta t} + s_{in}\int_0^t b_2 e^{-\vartheta(t-s)}\,ds \end{aligned}$$

Random disturbances on the input flow

$$= \quad p_0 e^{-\vartheta t} + \frac{s_{in} b_2}{\vartheta} \left[1 - e^{-\vartheta t}\right], \tag{2.27}$$

since $D + \alpha z^*_{\beta,\nu}(\theta_s \omega) \leq b_2$ for every $s \in \mathbb{R}$.

As a consequence, after making t go to infinity in (2.27), we have

$$\lim_{t \to +\infty} p(t; 0, \omega, p_0) \leq \frac{s_{in} b_2}{\vartheta}. \tag{2.28}$$

From (2.28) we know that, for every initial value $p_0 \in F$ and any given $\varepsilon > 0$, there exists some time $T_F(\omega, \varepsilon) > 0$ such that

$$0 \leq p(t; 0, \omega, p_0) \leq \frac{s_{in} b_2}{\vartheta} + \varepsilon$$

for all $t \geq T_F(\omega, \varepsilon)$. Thus,

$$B_\varepsilon = \left\{ (s, x_1, x_2) \in \mathscr{X} : s + \frac{m}{c}(x_1 + x_2) \leq \frac{s_{in} b_2}{\vartheta} + \varepsilon \right\}$$

is, for any $\varepsilon > 0$, a deterministic compact absorbing set (forwards in time) for the solutions of system (2.22)-(2.24).

□

Therefore, thanks to Theorem 2.3.2, it can be easily deduced that

$$B_0 := \left\{ (s, x_1, x_2) \in \mathscr{X} : s + \frac{m}{c}(x_1 + x_2) \leq \frac{s_{in} b_2}{\vartheta} \right\} \tag{2.29}$$

is a deterministic attracting set (forwards in time) for the solutions of the chemostat model with wall growth (2.22)-(2.24).

2.3.3 Internal structure of the deterministic attracting set

In this section, our aim is to analyze the internal structure of the deterministic attracting set B_0, given by (2.29). To this end, we perform the usual variable change when studying the chemostat model with wall growth by defining two new state variables, the total biomass and the proportion of the microorganisms in the medium, respectively, as follows

$$x(t) = x_1(t) + x_2(t) \qquad \text{and} \qquad \xi(t) = \frac{x_1(t)}{x_1(t) + x_2(t)}. \tag{2.30}$$

For the sake of simplicity, we will write x and ξ instead of $x(t)$ and $\xi(t)$.

From (2.30), by differentiation, we obtain the following random differential system

$$\frac{ds}{dt} = \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)(s_{in} - s) - \frac{ms}{a+s}x + b\nu\xi x, \tag{2.31}$$

$$\frac{dx}{dt} = -\nu x - \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)\xi x + \frac{cs}{a+s}x, \tag{2.32}$$

$$\frac{d\xi}{dt} = -\left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)\xi(1-\xi) - r_1\xi + r_2(1-\xi). \tag{2.33}$$

We remark that the dynamics of the proportion of the species in the liquid media, ξ, is uncoupled of the rest of the system, then we first analyze its asymptotic behavior and we investigate the rest of the system in a second step.

Thanks to (2.30), it is straightforward to prove by definition that

$$0 \leq \xi(t;0,\omega,\xi_0) \leq 1$$

for every $t \geq 0$ and any initial value $\xi_0 \in (0,1)$. In addition, from (2.33), we can evaluate the corresponding random differential equation when $\xi = 0$ and $\xi = 1$, respectively, such that we obtain

$$\left.\frac{d\xi}{dt}\right|_{\xi=0} = r_2 > 0 \qquad \text{and} \qquad \left.\frac{d\xi}{dt}\right|_{\xi=1} = -r_1 < 0,$$

whence we notice that the interval $(0,1) \subset \mathbb{R}$ defines a positively invariant set for the dynamics of the proportion.

On the one hand, thanks to the fact that $b_1 < D + \alpha z^*_{\beta,\nu}(\theta_t\omega) < b_2$ for every $t \in \mathbb{R}$, from (2.33) we have

$$\begin{aligned}\frac{d\xi}{dt} &= -\left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)\xi(1-\xi) - r_1\xi + r_2(1-\xi)\\ &\leq -(b_1 + r_1 + r_2)\xi + b_1 + r_2,\end{aligned}$$

hence we obtain the following random differential equation

$$\frac{d\xi}{dt} \leq -(b_1 + r_1 + r_2)\xi + b_1 + r_2. \tag{2.34}$$

By solving now (2.34), we obtain the following upper bound

$$\xi(t;0,\omega,\xi_0) \leq \xi_0 e^{-(b_1+r_1+r_2)t} + \frac{b_1 + r_2}{b_1 + r_1 + r_2}\left[1 - e^{-(b_1+r_2+r_2)t}\right]$$

for any initial value $\xi_0 \in (0,1)$ and for all $t \geq 0$.

On the other hand, from (2.33) we also have

$$\begin{aligned}\frac{d\xi}{dt} &= -\left(D+\alpha z^{*}_{\beta,\nu}(\theta_t\omega)\right)\xi(1-\xi)-r_1\xi+r_2(1-\xi)\\ &\geq -(b_2+r_1+r_2)\xi+r_2,\end{aligned}$$

whence we obtain

$$\frac{d\xi}{dt}\geq -(b_2+r_1+r_2)\xi+r_2. \tag{2.35}$$

By solving in this case (2.35), we obtain the following lower bound

$$\xi(t;0,\omega,\xi_0)\geq \xi_0 e^{-(b_2+r_1+r_2)t}+\frac{r_2}{b_2+r_1+r_2}\left[1-e^{-(b_2+r_1+r_2)t}\right]$$

for any initial value $\xi_0\in(0,1)$ and for all $t\geq 0$.

From the calculations above, we have the following bounds for the dynamics of the proportion ξ, which are given by

$$\xi(t;0,\omega,\xi_0)\leq \xi_0 e^{-(b_1+r_1+r_2)t}+\frac{b_1+r_2}{b_1+r_1+r_2}\left[1-e^{-(b_1+r_2+r_2)t}\right]. \tag{2.36}$$

and

$$\xi(t;0,\omega,\xi_0)\geq \xi_0 e^{-(b_2+r_1+r_2)t}+\frac{r_2}{b_2+r_1+r_2}\left[1-e^{-(b_2+r_1+r_2)t}\right] \tag{2.37}$$

for any initial value $\xi_0\in(0,1)$ and for all $t\geq 0$.

Then, by making t go to infinity in (2.36) and (2.37), respectively, we obtain

$$\frac{r_2}{b_2+r_1+r_2}\leq \lim_{t\to+\infty}\xi(t;0,\omega,\xi_0)\leq \frac{b_1+r_2}{b_1+r_1+r_2}$$

for every any initial value $\xi_0\in(0,1)$.

Hence, for any given $\varepsilon>0$ and any initial value $\xi_0\in(0,1)$, there exists some time $T(\omega,\varepsilon)>0$ such that

$$-\varepsilon+\frac{r_2}{b_2+r_1+r_2}\leq \xi(t;0,\omega,\xi_0)\leq \frac{b_1+r_2}{b_1+r_1+r_2}+\varepsilon$$

for all $t\geq T(\omega,\varepsilon)$.

Thus,

$$B^{\xi}_{\varepsilon}=\left\{\xi\in(0,1):-\varepsilon+\xi^{*}_{l}\leq\xi\leq\xi^{*}_{u}+\varepsilon\right\}$$

defines a deterministic compact absorbing set for the dynamics of the proportion, where ξ^{*}_{l} and ξ^{*}_{u} are

both deterministic constants given by

$$\xi_l^* := \frac{r_2}{b_2 + r_1 + r_2} \qquad \text{and} \qquad \xi_u^* := \frac{b_1 + r_2}{b_1 + r_1 + r_2}. \tag{2.38}$$

As a consequence, the dynamics of the proportion remains asymptotically inside B_ε^ξ for any given $\varepsilon > 0$ and, then, we obtain the following attracting set for the corresponding state variable describing the dynamics of the proportion

$$B_0^\xi := \left\{\xi \in (0,1) : \xi_l^* \leq \xi \leq \xi_u^*\right\}. \tag{2.39}$$

We remark that, since the constants defined in (2.38) are deterministic, both B_ε^ξ and B_0^ξ are also deterministic sets, i.e., they do not depend on the noise. In addition, they are absorbing sets forwards in time.

Remark 2.3.1 *We recall that $b_1 \leq D + \alpha z^*_{\beta,\nu}(\theta_t\omega) \leq b_2$ holds true for every $t \in \mathbb{R}$, thanks to the new framework previously set in Section 2.1.*

Now, we focus on the analysis of the dynamics of the substrate, s, and the microorganisms concentration, x. We already proved that, for every time t large enough, the dynamics of the proportion satisfies the following inequalities

$$\xi_l^* \leq \xi(t;0,\omega,\xi_0) \leq \xi_u^* \tag{2.40}$$

for every initial value $\xi_0 \in (0,1)$.

Having reached this point, we will define a new state variable

$$z(t) = cs(t) + mx(t).$$

We will write z, instead of $z(t)$, for the sake of simplicity.

Hence, by differentiation, due to the fact that $b \leq 1$, $c \leq m$ and since $\xi(t;0,\omega,\xi_0) \leq 1$ for every $t \geq 0$ and any initial value $\xi_0 \in (0,1)$, thanks to (2.40), we obtain that z satisfies the following random differential equations

$$\frac{dz}{dt} \leq -\left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)\xi_l^* z + cs_{in}\left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) \tag{2.41}$$

and

$$\frac{dz}{dt} \geq -\left[\nu + \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) - \frac{cb\nu}{m}\xi_l^*\right] z + c\left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right) s_{in} \tag{2.42}$$

for every time t large enough.

By solving now (2.41) and (2.42), thanks to Remark 2.3.1, we obtain

$$z(t;0,\omega,z_0) \quad \leq \quad z_0 e^{-D\xi_l^* t - \alpha\xi_l^* \int_0^t z^*(\theta_r\omega)dr}$$

Random disturbances on the input flow

$$+cs_{in}\int_0^t \left(D+\alpha z^*_{\beta,\nu}(\theta_s\omega)\right) e^{-D\xi_l^*(t-s)-\alpha\xi_l^*\int_s^t z^*(\theta_r\omega)dr}\,ds$$

$$\leq \quad z_0 e^{-b_1\xi_l^* t}+\frac{cs_{in}b_2}{\xi_l^* b_1}\left[1-e^{-\xi_l^* b_1 t}\right] \tag{2.43}$$

and

$$\begin{aligned} z(t;0,\omega,z_0) \quad &\geq \quad z_0 e^{-\left(\nu+D-\frac{cb\nu}{m}\xi_l^*\right)t-\alpha\int_0^t z^*(\theta_r\omega)dr} \\ &\quad +cs_{in}\int_0^t \left(D+\alpha z^*_{\beta,\nu}(\theta_s\omega)\right) e^{-\left(\nu+D-\frac{cb\nu}{m}\xi_l^*\right)(t-s)-\alpha\int_s^t z^*(\theta_r\omega)dr}\,ds \\ &\geq \quad z_0 e^{-\left(b_2+\nu-\frac{cb\nu}{m}\xi_l^*\right)t}+\frac{cs_{in}b_1}{b_2+\nu-\frac{cb\nu}{m}\xi_l^*}\left[1-e^{-\left(b_2+\nu-\frac{cb\nu}{m}\xi_l^*\right)t}\right], \end{aligned} \tag{2.44}$$

respectively, for every time t large enough.

Thus, after making t go to infinity in (2.43) and (2.44), we have

$$z_l^* := \frac{cs_{in}b_1}{b_2+\nu-\frac{cb\nu}{m}\xi_l^*} \leq \lim_{t\to+\infty} z(t;0,\omega,z_0) \leq \frac{cs_{in}b_2}{\xi_l^* b_1} =: z_u^*, \tag{2.45}$$

for every initial value $v_0 \in F$, where we used the fact that $b_2+\nu-\frac{cb\nu}{m}\xi_l^* > 0$ is fulfilled.

We would like to remark that both constants z_l^* and z_u^* in (2.45) do not depend on the noise ω or, in oder words, we obtained in (2.45) upper and lower deterministic bounds for the dynamics of z, what is more, forwards in time.

From (2.45), we have that, for every $v_0 \in F$ and any $\varepsilon > 0$, there exists some time $T_F(\omega,\epsilon) > 0$ such that

$$z_l^* - \varepsilon \leq z(t;0,\omega,z_0) \leq z_u^* + \varepsilon \tag{2.46}$$

holds true for all $t \geq T_F(\omega,\varepsilon)$.

As a result, we deduce that, for any $\varepsilon > 0$,

$$B_\varepsilon^{(s,x)} := \left\{(s,x)\in\mathbb{R}^2_+ : z_l^* - \varepsilon \leq cs+mx \leq z_u^*+\varepsilon\right\} \tag{2.47}$$

is a deterministic compact absorbing set (forwards in time) for the solutions of system (2.31)-(2.32).

Therefore, we obtain the following attracting set (forwards in time) for the solutions of system (2.31)-(2.32)

$$B_0^{(s,x)} := \left\{(s,x)\in\mathbb{R}^2_+ : z_l^* \leq cs+mx \leq z_u^*\right\},$$

see Figure 2.13.

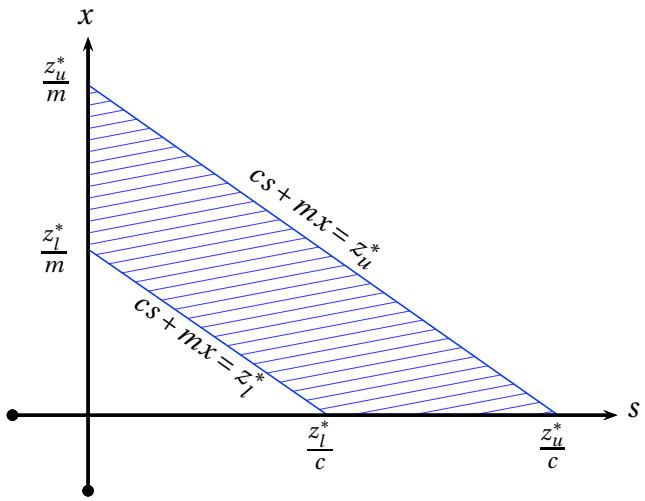


Figure 2.13: Attracting set $B_0^{(s,x)}$

Now we analyze the dynamics of both the nutrient and the species individually in order to obtain more detailed information about the long-time behavior of the random system (2.31)-(2.32). In addition, we will provide conditions under which the persistence in the *strong* sense (11) of both species, the ones in the medium and the ones sticked on the walls of the culture vessel, can be proved.

Proposition 2.3.1 *Assume that the following condition*

$$\nu + D\xi_l^* > c \tag{2.48}$$

holds true. Then, the attracting set for the solutions of the chemostat model with wall growth (2.22)-(2.24) *is reduced to a deterministic segment, more precisely, it is*

$$\widehat{B}_0^{(s,x)} = \left[\frac{z_l^*}{c}, \frac{z_u^*}{c}\right] \times \{0\} \times \{0\}.$$

Proof. On the one hand, from (2.32) we have that x satisfies the following random differential inequality

$$\frac{dx}{dt} \leq -\left[\nu + \left(D + \alpha z_{\beta,\nu}^*(\theta_t\omega)\right)\xi_l^* - c\right]x,$$

for every time t large enough, whose solution is given by

$$x(t;0,\omega,x_0) \leq x_0 e^{-(\nu+D\xi_l^*-c)t-\alpha\xi_l^*\int_0^t z_{\beta,\nu}^*(\theta_s\omega)ds}. \tag{2.49}$$

Besides, from (2.49), we have that

$$\lim_{t\to+\infty} x(t;0,\omega,x_0) \leq 0$$

as long as (2.48) is fulfilled or, in other words, both species become extinct if (2.48) holds true.

On the other hand, from (2.32) we also obtain the following random differential inequality

$$\frac{dx}{dt} \geq -\left(D\xi_u^* + \nu + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)x,$$

for every time t large enough, whose solution is given by

$$x(t;0,\omega,x_0) \geq x_0 e^{-(D\xi_u^*+\nu)t-\alpha\xi_u^*\int_0^t z^*_{\beta,\nu}(\theta_s\omega)ds}.$$

Thus, since $D\xi_u^* + \nu$ is always positive, we have

$$\lim_{t\to+\infty} x(t;0,\omega,x_0) \geq 0$$

for every initial value $v_0 \in F$, which does not provide us any extra information.

□

The next result gives us a condition under which the persistence of the microorganisms in the strong sense (11) can be proved.

Theorem 2.3.3 *Assume that*

$$\nu + b_2 < \frac{z_l^*}{a + \frac{z_u^*}{c}} \tag{2.50}$$

is fulfilled and (2.48) *does not hold, where we recall that z_l^* and z_u^* are the constants defined as*

$$z_l^* := \frac{cs_{in}b_1}{b_2 + \nu - \frac{cb\nu}{m}\xi_l^*} \qquad \text{and} \qquad z_u^* := \frac{cs_{in}b_2}{\xi_l^* b_1}.$$

Then, there exists a deterministic compact absorbing set, which is strictly contained in the first quadrant of the two-dimensional space, for the solutions of system (2.31)-(2.32).

Proof. Let us recall the random differential equation describing the dynamics of the microorganisms concentration, $x = x_1 + x_2$, which is given by

$$\frac{dx}{dt} = -\nu x - \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)\xi x + \frac{cs}{a+s}x,$$

whence we obtain that

$$\frac{dx(t;0,\omega,x_0)}{dt} = -\nu x(t;0,\omega,x_0) - \left(D + \alpha z^*_{\beta,\nu}(\theta_t\omega)\right)\xi(t;0,\omega,\xi_0)x(t;0,\omega,x_0)$$

$$+\frac{cs(t;0,\omega,s_0)}{a+s(t;0,\omega,s_0)}x(t;0,\omega,x_0). \tag{2.51}$$

On the one hand, thanks to the definition of the proportion (2.30), we have that

$$0 \leq \xi(t;0,\omega,\xi_0) \leq 1 \tag{2.52}$$

for every $t \geq 0$ and any initial value $\xi_0 \in (0,1)$.

Thus, from (2.51), thanks to the previous calculations and Remark 2.3.1, we obtain the following random differential inequality

$$\begin{aligned}\frac{dx(t;0,\omega,x_0)}{dt} &\geq -\nu x(t;0,\omega,x_0) - b_2 x(t;0,\omega,x_0) \\ &\quad +\frac{cs(t;0,\omega,s_0)}{a+s(t;0,\omega,s_0)}x(t;0,\omega,x_0)\end{aligned} \tag{2.53}$$

for all $t \geq 0$ and every initial value $\nu_0 \in F$.

By definition, we know that

$$z(t;0,\omega,z_0) = cs(t;0,\omega,s_0) + mx(t;0,\omega,x_0)$$

and, thanks to (2.46), we have that, for each $\nu_0 \in F$ and any $\varepsilon > 0$, there exists some time $T_F(\omega,\varepsilon) > 0$ such that

$$z_l^* - \varepsilon \leq cs(t;0,\omega,s_0) + mx(t;0,\omega,x_0) \leq z_u^* + \varepsilon$$

holds true for every $t \geq T_F(\omega,\varepsilon)$.

As a consequence, since $c \leq m$, we have the following inequalities

$$cs(t;0,\omega,s_0) \geq z_l^* - \varepsilon - mx(t;0,\omega,x_0)$$

and

$$s(t;0,\omega,s_0) \leq \frac{z_u^*}{c} + \frac{\varepsilon}{c} - x(t;0,\omega,x_0)$$

for every initial value $\nu_0 \in F$, any $\varepsilon > 0$ and for all $t \geq T_F(\omega,\varepsilon)$.

Then, from (2.53), we have

$$\begin{aligned}\frac{dx(t;0,\omega,x_0)}{dt} &\geq -\nu x(t;0,\omega,x_0) - b_2 x(t;0,\omega,x_0) \\ &\quad +\frac{z_l^* - mx(t;0,\omega,x_0) - \varepsilon}{a+\frac{z_u^*}{c}+\frac{\varepsilon}{c}-x(t;0,\omega,x_0)}x(t;0,\omega,x_0)\end{aligned} \tag{2.54}$$

for every $v_0 \in F$, any $\varepsilon > 0$ and for all $t \geq T_F(\omega, \varepsilon)$.

Now, we study the differential equation (2.54) when $x = \widetilde{x}$, where $\widetilde{x}$ is defined as

$$\widetilde{x} = \frac{z_l^* - (\nu + b_2)\left(a + \frac{z_u^*}{c}\right)}{m + c}. \tag{2.55}$$

Then, from (2.54) and considering $\varepsilon < c\widetilde{x}$, we obtain

$$\begin{aligned} \left.\frac{dx(t;0,\omega,x_0)}{dt}\right|_{x=\widetilde{x}} &\geq \left[-(\nu + b_2) + \frac{z_l^* - m\widetilde{x} - \varepsilon}{a + \frac{z_u^*}{c} + \frac{\varepsilon}{c} - \widetilde{x}}\right]\widetilde{x} \\ &> \left[-(\nu + b_2) + \frac{z_l^* - m\widetilde{x} - c\widetilde{x}}{a + \frac{z_u^*}{c} + \frac{c\widetilde{x}}{c} - \widetilde{x}}\right]\widetilde{x} = 0 \end{aligned}$$

for every $v_0 \in F$, any $\varepsilon \in (0, c\widetilde{x})$ and for all $t \geq T_F(\omega, \varepsilon)$.

Hence, as long as (2.50) is fulfilled, we have that, for any $\varepsilon \in (0, c\widetilde{x})$, where $\widetilde{x}$ is given by (2.55), for every $v_0 \in F$, there exists some time $T_F(\omega, \varepsilon) > 0$ such that

$$\left.\frac{dx(t;0,\omega,x_0)}{dt}\right|_{x=\widetilde{x}} > 0 \tag{2.56}$$

for all $t \geq T_F(\omega, \varepsilon)$.

Therefore, from (2.56) we conclude that, as long as (2.50) is fulfilled, we have the following lower deterministic bound for the dynamics of the species

$$x(t;0,\omega,x_0) > \widetilde{x},$$

for any $\varepsilon \in (0, c\widetilde{x})$, every given $v_0 \in F$ and for all $t \geq T_F(\omega, \varepsilon)$.

Now, let us recall the random differential equation held by the substrate

$$\frac{ds}{dt} = \left(D + \alpha z_{\beta,\nu}^*(\theta_t\omega)\right)(s_{in} - s) - \frac{ms}{a + s}x + b\nu\xi x$$

for every $t \geq 0$, whence we obtain that

$$\begin{aligned} \frac{ds(t;0,\omega,s_0)}{dt} &= \left(D + \alpha z_{\beta,\nu}^*(\theta_t\omega)\right)s_{in} - \left(D + \alpha z_{\beta,\nu}^*(\theta_t\omega)\right)s(t;0,\omega,s_0) \\ &\quad - \frac{ms(t;0,\omega,s_0)}{a + s(t;0,\omega,s_0)}x(t;0,\omega,x_0) \end{aligned}$$

$$+bv\xi(t;0,\omega,\xi_0)x(t;0,\omega,x_0), \tag{2.57}$$

for all $t \geq 0$ and every initial value $v_0 \in F$.

Moreover, from (2.46) and (2.52), we know that, for each $v_0 \in F$ and any $\varepsilon > 0$, there exists some time $T_F(\omega,\varepsilon) > 0$ such that

$$x(t;0,\omega,x_0) \leq \frac{z_u^*}{m} + \frac{\varepsilon}{m}$$

holds true for every $t \geq T_F(\omega,\varepsilon)$.

Summing up, thanks to the previous calculations, from (2.57) we have

$$\begin{aligned} \frac{ds(t;0,\omega,s_0)}{dt} &\geq b_1 s_{in} - b_2 s(t;0,\omega,s_0) \\ &\quad - \frac{ms(t;0,\omega,s_0)}{a + s(t;0,\omega,s_0)} \frac{z_u^* + \varepsilon}{m}, \end{aligned} \tag{2.58}$$

for every $v_0 \in F$, any $\varepsilon > 0$ and for all $t \geq T_F(\omega,\varepsilon)$.

Now, we study the differential equation (2.58) when $s = \widetilde{s}$, where $\widetilde{s}$ is defined as

$$\widetilde{s} = \frac{b_1 s_{in}}{b_2 + 2\frac{z_u^*}{a}}. \tag{2.59}$$

Then, from (2.58) and considering $\varepsilon < z_u^*$, we obtain

$$\begin{aligned} \left.\frac{ds(t;0,\omega,s_0)}{dt}\right|_{s=\widetilde{s}} &\geq b_1 s_{in} - b_2\widetilde{s} - \frac{\widetilde{s}}{a+\widetilde{s}}(z_u^* + \varepsilon) \\ &> b_1 s_{in} - b_2\widetilde{s} - \frac{2\widetilde{s}}{a} z_u^* = 0 \end{aligned}$$

for every $v_0 \in F$, any $\varepsilon \in (0, z_u^*)$ and for all $t \geq T_F(\omega,\varepsilon)$.

Hence, we have that, for any $\varepsilon \in (0, z_u^*)$ and every $v_0 \in F$, there exists some time $T_F(\omega,\varepsilon) > 0$ such that

$$\left.\frac{ds(t;0,\omega,s_0)}{dt}\right|_{s=\widetilde{s}} > 0$$

for all $t \geq T_F(\omega,\varepsilon)$.

Thus, we obtain the following lower deterministic bound for the dynamics of the substrate

$$s(t;0,\omega,s_0) > \widetilde{s},$$

for any $\varepsilon \in (0, z_u^*)$, every given $v_0 \in F$ and for all $t \geq T_F(\omega, \varepsilon)$.

In conclusion, we obtain that, by taking any $\varepsilon \in (0, \min\{c\widetilde{x}, z_u^*\})$, where $\widetilde{x}$ is given by (2.55), for every given $v_0 \in F$, there exists some time $T_F(\omega, \varepsilon) > 0$ such that

$$x(t; 0, \omega, x_0) > \widetilde{x} \tag{2.60}$$

and

$$s(t; 0, \omega, s_0) > \widetilde{s} \tag{2.61}$$

hold true for all $t \geq T_F(\omega, \varepsilon)$.

As a result, we can deduce that, for any $\varepsilon \in (0, \min\{c\widetilde{x}, z_u^*\})$,

$$\widehat{B}_\varepsilon^{(s,x)} = \left\{(s, x) \in \mathbb{R}_+^2 : x \geq \widetilde{x},\ s \geq \widetilde{s},\ z_l^* - \varepsilon \leq cs + mx \leq z_u^* + \varepsilon\right\}, \tag{2.62}$$

where $\widetilde{x}$ and $\widetilde{s}$ are defined by (2.55) and (2.59), respectively, is a deterministic compact absorbing set (forwards in time) for the solutions of system (2.31)-(2.32).

□

It is worth mentioning that we already proved the dynamics of system (2.31)-(2.32) to remain inside $B_\varepsilon^{(s,x)}$, defined as in (2.47), forwards in time. In the previous result, as long as (2.50) is fulfilled, we obtain in addition a smaller deterministic compact absorbing set $\widetilde{B}_\varepsilon^{(s,x)}$ forwards in time as well, defined by (2.62), which besides is strictly contained in the first quadrant of the two-dimensional space. This fact will be the main key, as already happened in the case without wall growth, to guarantee the persistence of both species, individually, in the strong sense (11).

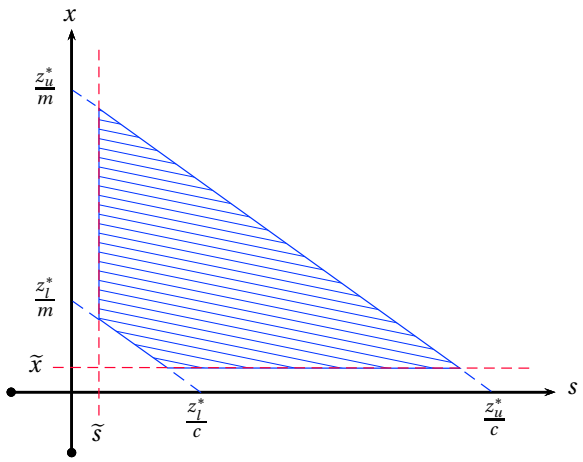


Figure 2.14: Attracting set $\widetilde{B}_0^{(s,x)}$

Therefore,

$$\widetilde{B}_0^{(s,x)} := \left\{(s,x) \in \mathbb{R}^2_+ \,:\, x \geq \widetilde{x},\ s \geq \widetilde{s},\ z_l^* \leq cs + mx \leq z_u^*\right\}$$

is a deterministic attracting set (forwards in time) for the solutions of system (2.31)-(2.32), see Figure 2.14.

Remark 2.3.2 *It is not difficult to check that both* $\widetilde{x} < \frac{z_l^*}{m}$ *and* $\widetilde{s} < \frac{z_l^*}{c}$ *are satisfied.*

Finally, we will analyze the dynamics of both species, x_1 and x_2, individually, to prove that both of them also persist as long as (2.50) holds true. To this end, thanks to , and the definition of the proportion, $\xi = x_1/x$, we obtain that

$$\begin{aligned} x_1(t;0,\omega,x_{10}) &= \xi(t;0,\omega,\xi_0)x(t;0,\omega,x_0) \\ &> \xi_l^*\widetilde{x} > 0 \end{aligned}$$

for every t large enough and any initial value $v_0 \in F$.

In addition, we also have

$$\begin{aligned} x_2(t;0,\omega,x_{20}) &= x(t;0,\omega,x_0)(1-\xi(t;0,\omega,\xi_0)) \\ &> (1-\xi_u^*)\widetilde{x} > 0 \end{aligned}$$

for every t large enough and any initial value $v_0 \in F$.

Hence, we obtain that both species, the ones in the medium and also the ones sticked on to the walls of the culture vessel, will persist as long as (2.50) holds true.

Remark 2.3.3 *It is possible to improve the deterministic lower bounds obtained in* (2.60) *and* (2.61) *by considering smaller values of* $\varepsilon > 0$. *Particularly, we could consider* $\varepsilon \in \left(0, \frac{c}{n}\widetilde{x}\right)$, *for any* $n \in \mathbb{N}$, *instead of* $\varepsilon \in (0, c\widetilde{x})$ *such that we get that* $x > \widetilde{x}_n$, *instead of* $x > \widetilde{x}$ *as in* (2.60), *where* $\widetilde{x}_n$ *is given by*

$$\widetilde{x}_n := \frac{z_l^* - (v+b_2)\left(a + \frac{z_u^*}{c}\right)}{m + \frac{c}{n}},$$

which clearly satisfies

$$\widetilde{x}_n := \frac{z_l^* - (v+b_2)\left(a + \frac{z_u^*}{c}\right)}{m + \frac{c}{n}} > \frac{z_l^* - (v+b_2)\left(a + \frac{z_u^*}{c}\right)}{m + c} =: \widetilde{x} > 0,$$

for any $n \in \mathbb{N}$, *since* $n \geq 1$.

Random disturbances on the input flow

Similarly, we could consider $\varepsilon \in \left(0, \frac{1}{n} z_u^*\right)$*, for any* $n \in \mathbb{N}$*, instead of* $\varepsilon \in (0, z_u^*)$ *such that we get* $s > \widetilde{s}_n$ *instead of* $s > \widetilde{s}$ *as in* (2.61)*, where* $\widetilde{s}_n$ *is given by*

$$\widetilde{s}_n := \frac{b_1 s_{in}}{b_2 + \frac{z_u^*}{a}\left(1 + \frac{1}{n}\right)}$$

which clearly verifies

$$\widetilde{s}_n := \frac{b_1 s_{in}}{b_2 + \frac{z_u^*}{a}\left(1 + \frac{1}{n}\right)} > \frac{b_1 s_{in}}{b_2 + \frac{2z_u^*}{a}} =: \widetilde{s} > 0,$$

for any $n \in \mathbb{N}$*, since* $n \geq 1$.

Summing up, in order to ensure the persistence of both species, the ones in the medium and the ones which are sticked on the walls of the culture vessel, the conditions to be imposed need to be the following ones

$$\nu < c - D\xi_l^* \qquad \text{and} \qquad \nu + b_2 < \frac{z_l^*}{a + \frac{z_u^*}{c}}, \tag{2.63}$$

where ξ_l^*, z_l^* and z_u^* are deterministic constants defined by (2.38) and (2.45), respectively.

We would like to highlight that both conditions in (2.63) essentially represent some restrictions on the dilution rate, on the disturbances on the input flow and also on the death collective rate, which is totally logical from the biological point of view.

In particular, if the dilution rate, or its equivalent input flow, were too large, then the microbial biomass would not be able to have access to the nutrient which would mean the extinction of both species and, furthermore, much more quantity of microbial biomass would be removed from the culture vessel to the collection vessel which would also increase significantly the probability of the extinction. In addition, the disturbances on the input flow cannot be too large since we want to avoid the drawbacks found when modeling the disturbances by means of the white noise. This is also the main reason which encouraged us to think about another kind of way to perturb the input flow in the chemostat model, particularly by using the Ornstein-Uhlenbeck process.

Apart from that, it made also us think about introducing this kind of stochastic processes when modeling other situations, such as the one with several species and different consumption functions or maybe other models different to the chemostat. To conclude, it is not surprising the presence of the death collective rate in both conditions (2.63) since it must be difficult to prove the persistence of both species if this parameter is too large. Therefore, the conditions required to get the persistence of both species are, as already pointed out, absolutely reasonable from the biological point of view.

2.3.4 Numerical simulations and final comments

In this section we show several numerical simulations for different values of the parameters involved in the random chemostat model with wall growth (2.22)-(2.24) in order to support the results provided

through this section. As made before, the blue dashed lines will represent the solution of the corresponding deterministic chemostat model whereas the other ones represent different realizations of the solution of the random system. Moreover, we display four different panels in each figure: there is a big one on the left-hand side showing the general dynamics of the model and there are three smaller panels on the right-hand side where the individual dynamics of the substrate and both species will be presented.

Firstly, we present several cases in which either the persistence of both species or the extinction is obtained and, eventually, we make a comparison between the random chemostat model with wall growth (2.22)-(2.24) and the one by perturbing the input flow by means of the standard Wiener process, which was already analyzed in Section 1.2 in Chapter 1, in order to show the differences between both ways of modeling the disturbances on the input flow in the chemostat model and remark the important advantages of using a bounded noise, in particular, the Ornstein-Uhlenbeck process.

On the one hand, we show some numerical simulations concerning the random chemostat model with wall growth (2.22)-(2.24). We consider in Figure 2.15 the following values of the different parameters involved in the model: $s_{in} = 4$, $D = 2$, $a = 1.6$, $m = 2$, $b = 0.5$, $\nu = 1.2$, $c = 3$, $r_1 = 0.2$, $r_2 = 0.4$, $\alpha = 0.5$, $\beta = 1$, $\nu = 0.2$ and we will take $s_0 = 2.5$, $x_{10} = 2$, $x_{20} = 2$ as initial values for the substrate and both species, respectively. As a result, we can see that both species persist.

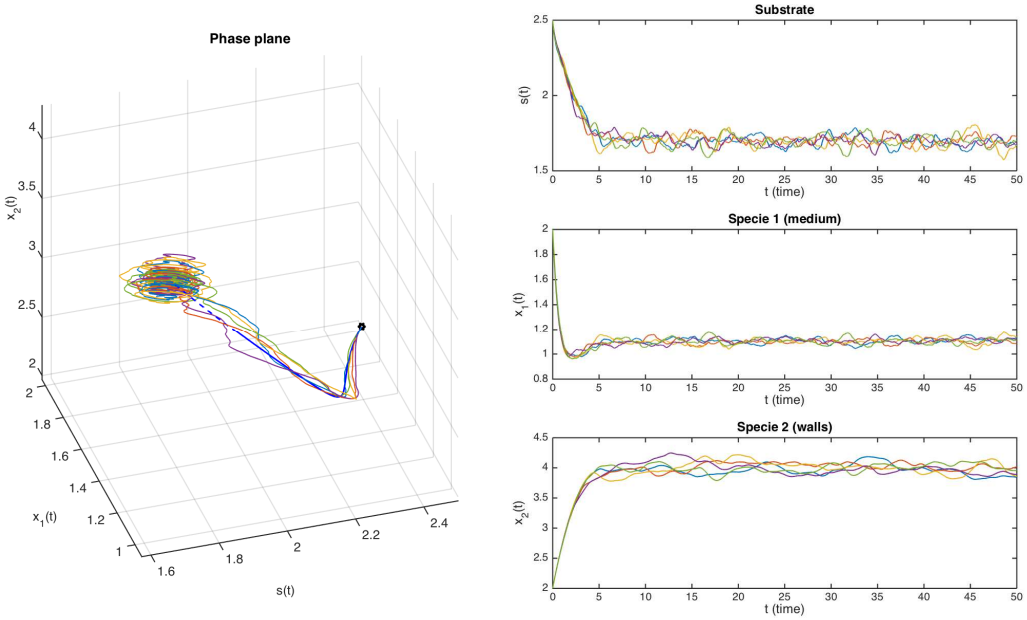


Figure 2.15: Persistence of the species in the random chemostat model with wall growth

Random disturbances on the input flow

In the sequel, we only refer to the parameters to be changed respect to the last ones used and we suppose the rest to be the same than before. For instance, in Figure 2.16 we will increase the quantity of noise to $\alpha = 2$, the mean reversion constant to $\beta = 4$ and the volatility constant to $\nu = 0.7$, respect to the parameters used in the last figure. We can observe that, even though the intensity of the noise is considerable large, we can still obtain the persistence of both species and we also remark that it could be inconceivable to consider such a large intensity of noise when using the standard Brownian motion without obtaining important drawbacks which would be, as explained in Chapter 1, totally unrealistic from the biological point of view.

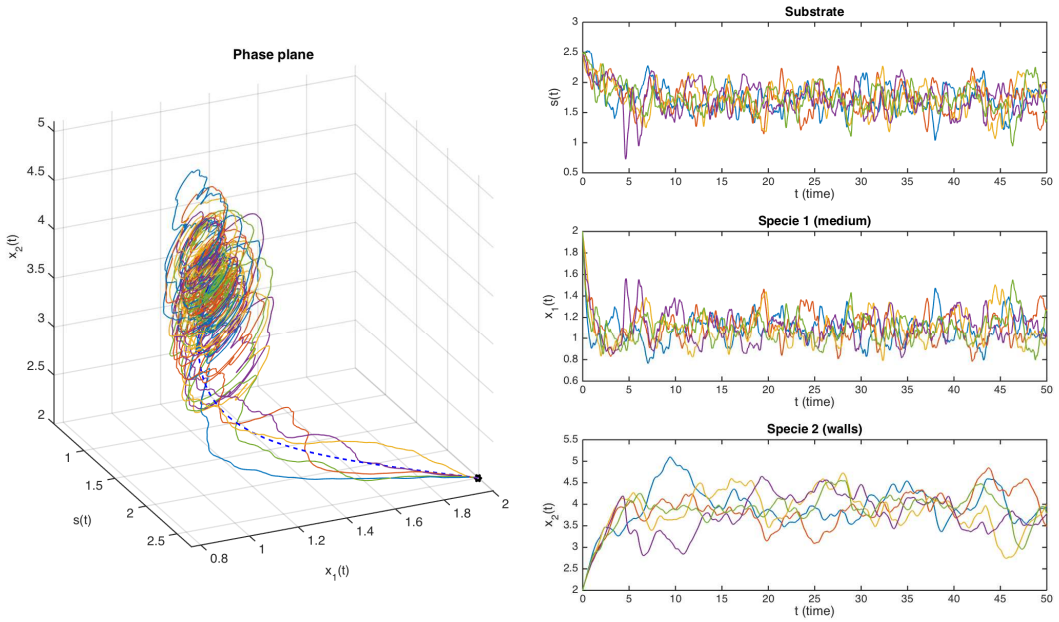


Figure 2.16: Persistence of the species in the random chemostat model with wall growth (ii)

On another hand, in Figure 2.17 we take $s_{in} = 4$, $D = 1.5$, $a = 1.6$, $m = 2$, $b = 1$, $\nu = 1.7$, $c = 2.4$, $r_1 = 0.6$, $r_2 = 0.4$, $\alpha = 0.5$, $\beta = 1$, $\nu = 0.2$ and we will take $s_0 = 2.5$, $x_{10} = 2$, $x_{20} = 2$ as initial values for the substrate and both species, respectively. Then, both species become extinct, as can be easily observed, which is quite logical in view of the values of the parameters, specially the collective death rate and the consumption rate of the species, which have been increased respect to the case of persistence.

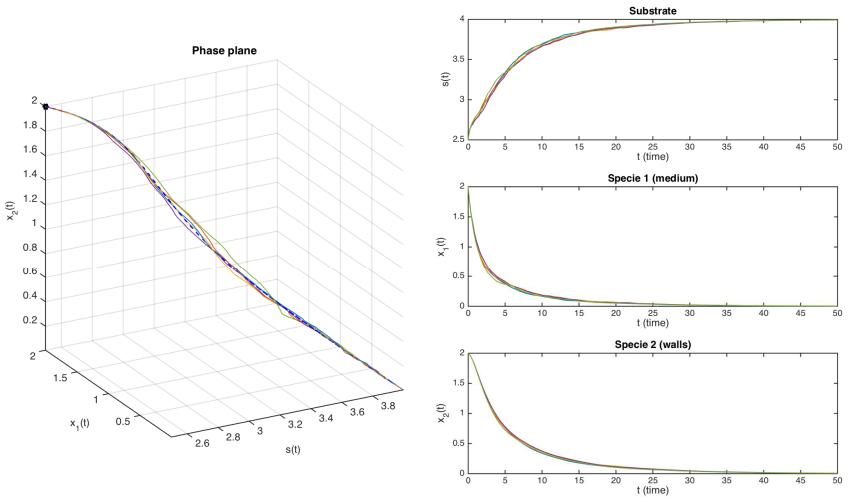


Figure 2.17: Extinction of the species in the random chemostat model with wall growth

Finally, in Figure 2.18 we increase the quantity of noise to $\alpha = 2$, the mean reversion constant to $\beta = 4$ and the volatility constant to $\nu = 0.7$ and we remark that the rest of the parameters do not change respect to the last ones in Figure 2.17. In this case we can also see easily that both species become extinct, which is not surprising by taking into account what happened in the last figure and the new values of the parameters involved in the disturbances.

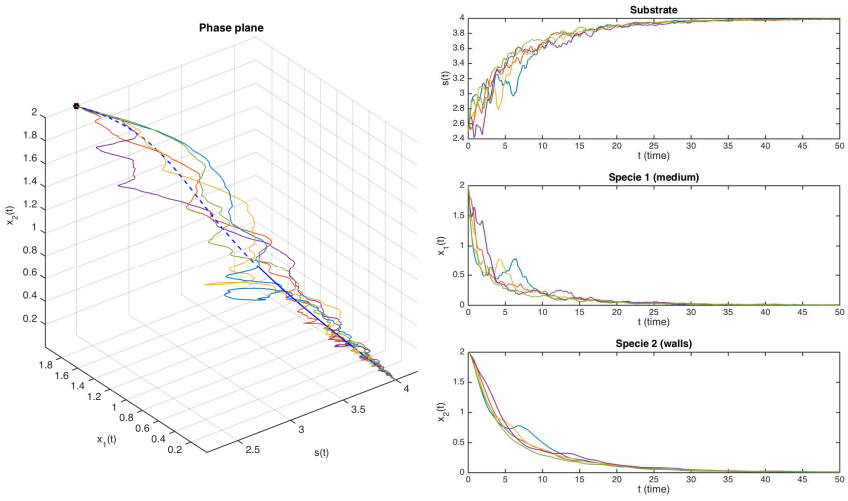


Figure 2.18: Extinction of the species in the random chemostat model with wall growth (ii)

Random disturbances on the input flow

Eventually, we present some numerical simulations where a typical realization of the stochastic chemostat model with wall growth, which was already analyzed in Section 1.2 in Chapter 1, and two typical ones of the random chemostat model with wall growth will be plotted together in order to see easily the differences of modeling the disturbances on the input flow in the chemostat model by using both the white noise (orange lines) and the Ornstein-Uhlenbeck process (red and green lines).

Firstly, in Figure 2.19 we take $s_{in} = 4$, $D = 2$, $a = 1.6$, $m = 2$, $b = 0.5$, $\nu = 1.2$, $c = 3$, $r_1 = 0.2$, $r_2 = 0.4$ and we consider $s_0 = 2.5$, $x_{10} = 2$, $x_{20} = 2$ as initial values for the substrate and both species, respectively. We also choose $\alpha = 0.8$, $\nu = 0.7$ and both $\beta = 2$ (red line) and $\beta = 1$ (green line). In this case, we can see that both species persist and we remark the huge disturbances obtained in case of using the white noise respect to the Ornstein-Uhlenbeck process, in fact, these disturbances can be also observed to affect to the specie x_2 even though it is not affected by the random input flow directly (see (2.24)), which do not happen when perturbing the input flow by means of the bounded noise.

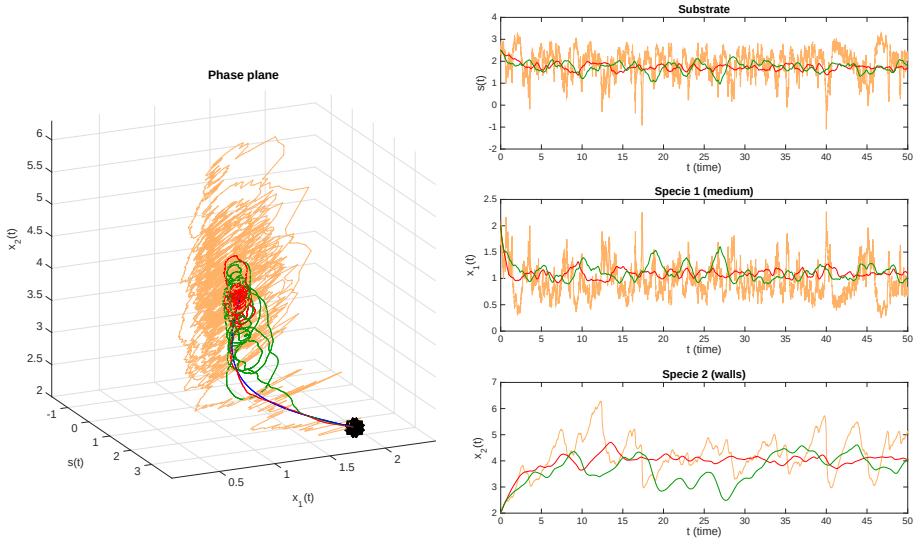


Figure 2.19: Comparison in case of persistence

Finally, in Figure 2.20 we take $s_{in} = 4$, $D = 1.5$, $a = 1.6$, $m = 2$, $b = 1$, $\nu = 1.7$, $c = 2.4$, $r_1 = 0.6$, $r_2 = 0.4$ and we consider $s_0 = 2.5$, $x_{10} = 2$, $x_{20} = 2$ as initial values for the substrate and both species, respectively. In this case we increase the quantity of noise, respect to the last case, to $\alpha = 1.5$, $\nu = 0.7$ and both $\beta = 2$ (red) and $\beta = 1$ (green). We can observe that both species become extinct and we remark again the significant disturbances when using the white noise respect to the case when considering the Ornstein-Uhlenbeck process.

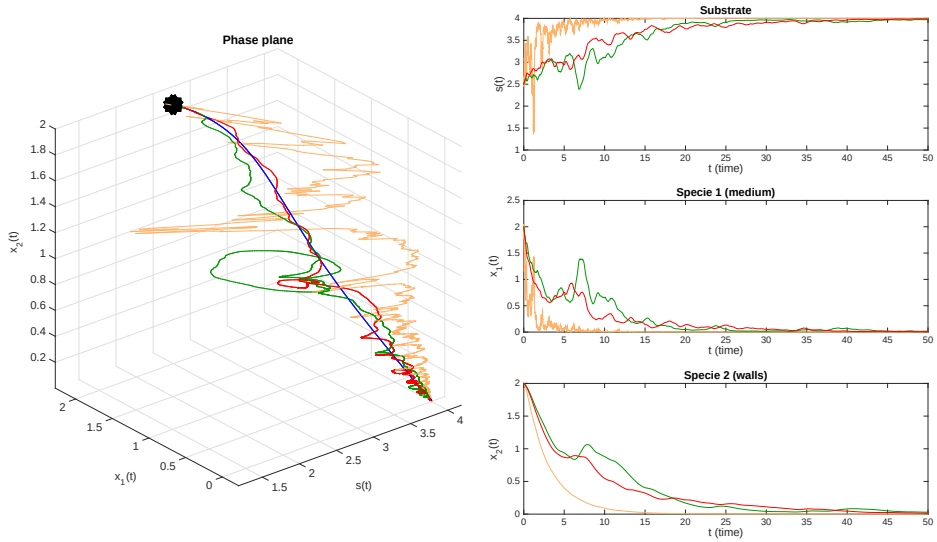


Figure 2.20: Comparison in case of extinction

CHAPTER 3

Modeling and analysis of environmental effects in chemostat models by means of the white noise

In this chapter we will investigate both chemostat models with and without wall growth where some stochastic disturbances are introduced, by means of the well-known standard Brownian motion, to model environmental effects. It clearly differs from the disturbances considered in the previous chapters where our main goal was to study the effects of random (Chapter 2) and stochastic (Chapter 1) disturbances on the input flow of chemostat models. This way of introducing stochasticity have already been used and motivated by several authors and, to sum up, the main, but not the only, advantage is that every state variable remain positive for any realization of the noise, something which is absolutely necessary when working with population dynamics. The existence and uniqueness of global solution will be proved and the theory of random dynamical systems and pullback attractors will be used to guarantee the existence and uniqueness of random pullback attractor. Eventually, several numerical simulations will be also shown to support the results proved through the whole chapter.

We would like to remark that the analysis carried out in this chapter is similar to the one in Chapter 1. Nevertheless, as in this case we consider another different way of modeling disturbances in the chemostat model, we prefer not to omit many calculations in order to make the readability easier. In addition, even though the analysis is similar, in this case the results clearly improve those presented in Chapter 1.

The results and explanations concerning the contributions of this chapter can be found in [10].

3.1 Stochastic chemostat model

Let us first recall the simplest deterministic chemostat model with Monod kinetics

$$\frac{ds}{dt} = (s_{in} - s)D - \frac{msx}{a+s}, \tag{3.1}$$

$$\frac{dx}{dt} = x\Big(\frac{ms}{a+s} - D\Big), \tag{3.2}$$

where $s(t)$ and $x(t)$ denote concentrations of the nutrient and the microbial biomass, respectively; s_{in} denotes the volumetric dilution rate, a is the half-saturation constant, D is the dilution rate and m is the maximal consumption rate of the nutrient and also the maximal specific growth rate of microorganisms. We notice that all parameters are positive and we use a function Holling type-II, which is defined as $\mu(s) = ms/(a+s)$, as functional response of the microorganism describing how the nutrient is consumed by the species.

Our aim in this chapter is to introduce stochasticity in system (3.1)-(3.2), by making use of the standard Wiener process, to model environment effects which are non-deterministic. In other words, we could write our model as

$$\frac{ds(t)}{dt} = s(t)f_1(s(t), x(t)),$$

$$\frac{dx(t)}{dt} = x(t)f_2(s(t), x(t)),$$

and then we could add some stochastic perturbation $\alpha_i \dot{W}_i$ to the functions $f_i(\cdot,\cdot)$, for $i \in \{1,2\}$, instead of adding it directly to ds/dt and dx/dt, as follows

$$\frac{ds(t)}{dt} = s(t)\left[f_1(s(t), x(t)) + \alpha_1 \dot{W}_1(t)\right],$$

$$\frac{dx(t)}{dt} = x(t)\left[f_2(s(t), x(t)) + \alpha_2 \dot{W}_2(t)\right],$$

or, equivalently,

$$ds(t) = s(t)f_1(s(t), x(t))dt + \alpha_1 s(t)dW_1(t),$$

$$dx(t) = x(t)f_2(s(t), x(t))dt + \alpha_2 x(t)dW_2(t).$$

In this way, the populations s and x will always remain positive for any realization of the Wiener processes W_i.

Moreover, in the paper by Imhof and Walcher (see [53]) the authors justify mathematically that it could

be reasonable to consider the following stochastic chemostat model

$$\begin{aligned} ds &= \left[(s_{in}-s)D-\frac{msx}{a+s}\right]dt+\alpha_1 s dW_1(t), \\ dx &= \left[-Dx+\frac{msx}{a+s}\right]dt+\alpha_2 x dW_2(t), \end{aligned}$$

where W_1 and W_2 are independent Wiener processes. To this end, a discrete Markov chain is considered for some increment δt and the convergence to the solution of the original stochastic equation is proved as δt tends to zero, whenever it exists a unique solution (see [53] for a more detailed explanation).

Motivated by this feature, in this chapter we consider a noisy term in each equation (3.1)-(3.2) in the same fashion as in [53], which ensures the positivity of both the nutrient and biomass, although does not preserve the washout equilibrium from the deterministic to the stochastic model. More precisely, we consider now the following system, which is understood in the Itō sense

$$\begin{aligned} ds &= \left[(s_{in}-s)D-\frac{msx}{a+s}\right]dt-\alpha s dW(t), \\ dx &= \left[-Dx+\frac{msx}{a+s}\right]dt-\alpha x dW(t), \end{aligned}$$

where $W(t)$ is a standard Brownian motion, and $\alpha \geq 0$ represents the intensity of noise.

We remark that, in order to make the calculations much more tractable and clear, we consider the same noise in both equations, even though a similar analysis could be developed by using different Brownian motions in each equation. This leads to more complicated technicalities that we prefer to avoid.

We would also like to note that there are not special reasons to consider the sign minus (−) in front of the stochastic terms, instead of the positive one used in [53], since the choice does not cause any effect over the behavior of our system.

Now, by using the well-known conversion between Itō and Stratonovich senses we obtain the following stochastic chemostat

$$ds = \left[-\bar{D}s-\frac{msx}{a+s}+s_{in}D\right]dt-\alpha s\circ dW(t), \tag{3.3}$$

$$dx = \left[-\bar{D}x+\frac{msx}{a+s}\right]dt-\alpha x\circ dW(t), \tag{3.4}$$

where

$$\bar{D} := D+\frac{\alpha^2}{2}. \tag{3.5}$$

Before analyzing the previous system, we would like to highlight some significant insights. We will only refer to the case without wall growth since similar ones hold for the other case as well. Concerning the de-

terministic chemostat model (DCM) given by (3.1)-(3.2), some authors have recently proved (see [15–17]) the existence of a unique axial equilibrium $(s_{in}, 0)$ which is asymptotically stable provided $D > m$, therefore this situation corresponds to the extinction of the microorganism. However, if $D < m$ and $aD/(m-D) < s_{in}$ the axial equilibrium becomes unstable and a unique positive globally asymptotically stable equilibrium appears inside the positive quadrant, i.e., persistence of the microorganism can be ensured. Notice that, in this case, the global attractor exists and consists of both equilibria and the heteroclinic solutions between them. Otherwise, no more information can be deduced related to the asymptotic behavior of the system.

Regarding the stochastic chemostat model (SCM) (3.3)-(3.4), we prove in this chapter that there exists a unique global random attractor which is given by singleton components $(s_{in}D\rho^*(\omega), 0)$ provided $D + \alpha^2/2 > m$ (see its definition in (3.12) in Section 3.1.3 for more details). Otherwise, the unique random pullback attractor is contained in a segment whose intersection with the axes $s = 0$ and $x = 0$ is reduced to two single points.

In light of the previous facts, observe that when $D < m$ and $aD/(m-D) < s_{in}$ we can choose α, large enough, such that $D + \alpha^2/2 > m$. This means that persistence of the microorganism holds for (DCM), while for (SCM) we have extinction since the random pullback attractor becomes the single random point $(s_{in}D\rho^*(\omega), 0)$. This fact is closely related to the stabilizing effects that Itō's noise can produce on deterministic systems. However, if we considered a Stratonovich interpretation for our perturbation at the beginning of our study, then we would have obtained D instead of $\bar{D}$ in (3.3)-(3.4); in other words, assumption $D + \alpha^2/2 > m$ in (SCM) would become $D > m$, the same that we had for (DCM). Consequently, no stabilizing effect is produced by the noise (see [8, 15, 51] and Remark 3.3 in [56] for a more detailed discussion on this topic). Thus, not only the type of noise but also its mathematical interpretation can provide different results, something that has to be taken into account by the modeler. A reference that could help to make the appropiate choice in a specific application is [73], where the author presents a criterion to determine which interpretation of the noise is the most useful in his work.

3.1.1 Stochastic chemostat becomes a random chemostat

In this section we will focus on investigating the stochastic system (3.3)-(3.4). To this end, similarly to the analysis carried out in Chapter 1, we will transform it into a differential system with random coefficients and without noise by using the stationary Ornstein-Uhlenbeck process z^* (see Appendix A for more information). Then, we first define the new variables σ and κ as follows

$$\sigma(t) = s(t)e^{\alpha z^*(\theta_t\omega)} \quad \text{and} \quad \kappa(t) = x(t)e^{\alpha z^*(\theta_t\omega)}. \tag{3.6}$$

For the sake of simplicity, and when no confusion is possible, we will write z^* instead of $z^*(\theta_t\omega)$, and σ and κ instead of $\sigma(t)$ and $\kappa(t)$.

Hence, by differentiation, it is straightforward that

$$\frac{d\sigma}{dt} = -(\bar{D} + \alpha z^*)\sigma - \frac{m\sigma e^{-\alpha z^*}}{a + \sigma e^{-\alpha z^*}}\kappa + s_{in} D e^{\alpha z^*}, \tag{3.7}$$

$$\frac{d\kappa}{dt} = -(\bar{D} + \alpha z^*)\kappa + \frac{m\sigma e^{-\alpha z^*}}{a + \sigma e^{-\alpha z^*}}\kappa. \tag{3.8}$$

3.1.2 Random chemostat generates a random dynamical system

Next we prove that the random chemostat (3.7)-(3.8) generates a random dynamical system. Henceforth, we denote the first quadrant by $\mathscr{X} := \{(x, y) \in \mathbb{R}^2,\ x \geq 0,\ y \geq 0\}$.

Theorem 3.1.1 *For any $\omega \in \Omega$ and any initial value $u_0 := (\sigma_0, \kappa_0) \in \mathscr{X}$, where σ_0 and κ_0 denote $\sigma(0; 0, \omega, u_0)$ and $\kappa(0; 0, \omega, u_0)$ respectively, the system* (3.7)-(3.8) *possesses a unique global solution*

$$u(\cdot; 0, \omega, u_0) := (\sigma(\cdot; 0, \omega, u_0), \kappa(\cdot; 0, \omega, u_0)) \in \mathscr{C}^1([0, \infty), \mathscr{X})$$

with $u(0; 0, \omega, u_0) = u_0$. Moreover the solution mapping generates a random dynamical system $\varphi_u : \mathbb{R}^+ \times \Omega \times \mathscr{X} \to \mathscr{X}$ defined as

$$\varphi_u(t, \omega)u_0 = u(t; 0, \omega, u_0), \quad \text{for all } t \in \mathbb{R}^+,\ u_0 \in \mathscr{X},\ \omega \in \Omega,$$

the value at time t of the solution of system (3.7)-(3.8) *with initial state u_0 at time zero.*

Proof. Observe that we can rewrite one of the terms in the previous equations as

$$\frac{m\sigma e^{-\alpha z^*}}{a + \sigma e^{-\alpha z^*}}\kappa = \frac{m\sigma e^{-\alpha z^*} + ma - ma}{a + \sigma e^{-\alpha z^*}}\kappa = m\kappa - \frac{ma}{a + \sigma e^{-\alpha z^*}}\kappa$$

and therefore system (3.7)-(3.8) turns into

$$\frac{d\sigma}{dt} = -(\bar{D} + \alpha z^*)\sigma - m\kappa + \frac{ma}{a + \sigma e^{-\alpha z^*}}\kappa + s_{in} D e^{\alpha z^*}, \tag{3.9}$$

$$\frac{d\kappa}{dt} = -(\bar{D} + \alpha z^*)\kappa + m\kappa - \frac{ma}{a + \sigma e^{-\alpha z^*}}\kappa. \tag{3.10}$$

Denoting $u(\cdot; 0, \omega, u_0) := (\sigma(\cdot; 0, \omega, u_0), \kappa(\cdot; 0, \omega, u_0))$, system (3.9)-(3.10) can be rewritten as

$$\frac{du}{dt} = L(\theta_t\omega)\ u + F(u, \theta_t\omega),$$

where

$$L(\theta_t\omega) = \begin{pmatrix} -(\bar{D} + \alpha z^*) & -m \\ 0 & -(\bar{D} + \alpha z^*) + m \end{pmatrix}$$

and $F : \mathscr{X} \times \Omega \longrightarrow \mathbb{R}^2$ is given by

$$F(\eta,\omega) = \begin{pmatrix} \dfrac{ma}{a+\eta_1 e^{-\alpha z^*(\omega)}}\eta_2 + Ds_{in}e^{\alpha z^*(\omega)} \\ \dfrac{-ma}{a+\eta_1 e^{-\alpha z^*(\omega)}}\eta_2 \end{pmatrix},$$

where $\eta = (\eta_1, \eta_2) \in \mathscr{X}$.

Since $t \mapsto z^*(\theta_t\omega)$ is continuous, L generates an evolution system on $\mathbb{R}^2$. Moreover, we notice that

$$\frac{\partial}{\partial\eta_1}\left[\pm\frac{ma}{a+\eta_1 e^{-\alpha z^*}}\eta_2 + \varrho\right] = \mp\frac{mae^{-\alpha z^*}}{(a+\eta_1 e^{-\alpha z^*})^2}\eta_2,$$

and

$$\frac{\partial}{\partial\eta_2}\left[\pm\frac{ma}{a+\eta_1 e^{-\alpha z^*}}\eta_2 + \varrho\right] = \pm\frac{ma}{a+\eta_1 e^{-\alpha z^*}},$$

where ϱ denotes a constant which does not depends on $(\eta_1, \eta_2) \in \mathscr{X}$, therefore $F(\cdot, \theta_t\omega) \in \mathscr{C}(\mathscr{X} \times [0,\infty); \mathbb{R}^2)$ and is continuously differentiable with respect to the variables (η_1, η_2), which implies that it is locally Lipschitz with respect to $(\eta_1, \eta_2) \in \mathscr{X}$.

Therefore, thanks to classical results from the theory of ordinary differential equations, system (3.9)-(3.10) possesses a unique local solution. Let us check now that in fact this solution is a global one.

We define $q(t) := \sigma(t) + \kappa(t)$ and thanks to (3.7)-(3.8) we have

$$\frac{dq}{dt} = -(\bar{D} + \alpha z^*)q + s_{in}De^{\alpha z^*}.$$

By solving the previous differential equation we obtain

$$q(t;0,\omega,q_0) = q_0 e^{-\bar{D}t - \alpha\int_0^t z^* ds} + s_{in}D\int_0^t e^{\alpha z^*} e^{-\bar{D}(t-s) - \alpha\int_s^t z^* dr} ds, \tag{3.11}$$

hence q is clearly bounded above by an expression which does not blow up.

On the other hand, from (3.7)

$$\frac{d\sigma}{dt} \leq -(\bar{D} + \alpha z^*)\sigma + s_{in}De^{\alpha z^*}.$$

Hence, similarly to previous calculations,

$$\sigma(t;0,\omega,\sigma_0) \leq \sigma_0 e^{-\bar{D}t - \alpha\int_0^t z^* ds} + s_{in}D\int_0^t e^{\alpha z^*} e^{-\bar{D}(t-s) - \alpha\int_s^t z^* dr} ds,$$

thus σ does not blow up either.

Summing up, we have proved that $q(t)$ and $\sigma(t)$ do not blow up and the same happens to $\kappa(t) = q(t) - \sigma(t)$. Therefore, the unique local solution to system (3.7)-(3.8) can be extended to a unique global one.

Now we would like to check that the global solution of (3.7)-(3.8) belongs to the first quadrant for any $t \geq 0$. From (3.7), if $\sigma(t) = 0$ for some $t^* \in \mathbb{R}^+$, we have

$$\frac{d\sigma}{dt}(t^*) = \left[-(\bar{D} + \alpha z^*)\sigma - \frac{m\sigma e^{-\alpha z^*}}{a + \sigma e^{-\alpha z^*}}\kappa + s_{in} D e^{\alpha z^*} \right](t^*) = s_{in} D e^{\alpha z^*} > 0.$$

Besides, given $(\sigma_0, 0)$ with $\sigma_0 > 0$, there exists a unique solution of system (3.7)-(3.8) satisfying $\sigma(t_0) = \sigma_0$ and $\kappa(t_0) = 0$ for some initial time $t_0 \geq 0$. Imposing $\kappa \equiv 0$ we deduce that σ is given by

$$\sigma(t; t_0, \omega, \sigma(t_0)) = \sigma(t_0) e^{-\bar{D}(t-t_0) - \alpha \int_{t_0}^t z^* ds} + s_{in} D \int_{t_0}^t e^{\alpha z^*} e^{-\bar{D}(t-s) - \alpha \int_s^t z^* dr} ds.$$

Now, let us pick $(\sigma_0, \kappa_0) \in \mathscr{X}$. Thus, there exists a unique solution $(\sigma(t), \kappa(t))$ such that $\sigma(0) = \sigma_0$ and $\kappa(0) = \kappa_0$. If there is some first $t^* > 0$ verifying $\kappa(t^*) = 0$, then we have that $(\sigma(\cdot), \kappa(\cdot))$ is the unique solution of system (3.7)-(3.8) with $\sigma(t^*) = \sigma^*$ and $\kappa(t^*) = 0$. Moreover $\kappa(t) > 0$ for all $0 \leq t < t^*$; however, we already have another solution $(\sigma(t), 0)$ for all $t \geq t^* - \delta$ (for any $\delta > 0$ small enough) for this problem, so we obtain a contradiction. As a result, we deduce that for any initial data $u_0 \in \mathscr{X}$ the solution remains in the first quadrant.

Now we can define the mapping $\varphi_u : \mathbb{R}^+ \times \Omega \times \mathscr{X} \to \mathscr{X}$ by

$$\varphi_u(t, \omega) u_0 := u(t; 0, \omega, u_0), \quad \text{for all } t \geq 0,\ u_0 \in \mathscr{X},\ \omega \in \Omega.$$

Since the function F is continuous in (u, t), and is measurable in ω, we obtain that the previous mapping is $(\mathscr{B}[0,\infty) \times \mathscr{F} \times \mathscr{B}(\mathscr{X}), \mathscr{B}(\mathscr{X}))-$measurable. It then follows that (3.7)-(3.8) generate the continuous random dynamical system $\{\varphi_u(t, \omega)\}_{t \geq 0, \omega \in \Omega}$.

□

3.1.3 Existence of the random pullback attractor

In this section we prove the existence and uniqueness of the random pullback attractor associated to the random chemostat (3.7)-(3.8), describing its internal structure explicitly.

Let us remember that $\mathscr{E}(\mathscr{X})$ denotes the set of all tempered sets in $\mathscr{X}$.

Proposition 3.1.1 *For any $\varepsilon > 0$, there exists a tempered compact random absorbing set $B_\varepsilon(\omega) \in \mathscr{E}(\mathscr{X})$ of the random dynamical system $\{\varphi_u(t, \omega)\}_{t \geq 0, \omega \in \Omega}$.*

Proof. Remember that $q = \sigma + \kappa$. Then, by replacing ω by $\theta_{-t}\omega$ in (3.11), we have

$$q(t;0,\theta_{-t}\omega,q_0) = q_0 e^{-\bar{D}t-\alpha\int_{-t}^{0} z^*(\theta_s\omega)ds} + s_{in}D\int_0^t e^{\tau\left[-\bar{D}+\frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau}-\frac{\alpha}{\tau}\int_{-\tau}^{0} z^*(\theta_r\omega)dr\right]}d\tau,$$

and therefore

$$\lim_{t\to+\infty} q(t;0,\theta_{-t}\omega,q_0) = s_{in}D\rho^*(\omega)$$

since $\bar{D}$ is always positive, where $\rho^*(\omega)$ is defined by

$$\rho^*(\omega) := \int_0^{\infty} e^{\tau\left[-\bar{D}+\frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau}-\frac{\alpha}{\tau}\int_{-\tau}^{0} z^*(\theta_r\omega)dr\right]}d\tau. \tag{3.12}$$

Note that the above integrand converges to zero when τ goes to infinity, but not the integral. Moreover, $\rho^*(\omega)$ has sub-exponential growth.

Therefore, for any given $\varepsilon > 0$ and each $u_0 \in E(\theta_{-t}\omega)$, there exists $T_E(\omega,\varepsilon) > 0$ such that

$$s_{in}D\rho^*(\omega) - \varepsilon \le q(t;0,\theta_{-t}\omega,q_0) \le s_{in}D\rho^*(\omega) + \varepsilon$$

for all $t \ge T_E(\omega,\varepsilon)$.

We now define

$$B_\varepsilon(\omega) := \left\{(\sigma,\kappa) \in \mathscr{X} : s_{in}D\rho^*(\omega) - \varepsilon \le \sigma + \kappa \le s_{in}D\rho^*(\omega) + \varepsilon\right\},$$

thus $B_\varepsilon(\omega) \in \mathscr{E}(\omega)$ is a tempered compact random absorbing set in $\mathscr{X}$ for any $\varepsilon > 0$.

□

Hence, from Proposition B.0.1 in Appendix B, the random dynamical system generated by the system (3.7)-(3.8) possesses a unique random attractor given by $\mathscr{A} = \{A(\omega)\}_{\omega\in\Omega} \subset B_\varepsilon(\omega)$ for any $\varepsilon > 0$. Thus $\mathscr{A} = \{A(\omega)\}_{\omega\in\Omega} \subset B_0(\omega)$, i.e., we have the following expression for each component of the attractor

$$A(\omega) := (s_{in}D\rho^*(\omega) - \kappa(\omega), \kappa(\omega)).$$

The following result provides information concerning the internal structure of the unique random pull-back attractor associated to the random chemostat (3.7)-(3.8).

Proposition 3.1.2 *For $\bar{D}$ defined by (3.5) assume that*

$$\bar{D} > m. \tag{3.13}$$

Then, the random attractor associated to the random dynamical system $\{\varphi_u(t,\omega)\}_{t\ge0,\omega\in\Omega}$ has the following structure:

$$\mathscr{A} = \{A(\omega)\}_{\omega\in\Omega}, \quad \textit{where} \quad A(\omega) = (s_{in}D\rho^*(\omega), 0).$$

Proof. Thanks to (3.8) we know that

$$\frac{d\kappa}{dt} \leq -(\bar{D} - m + \alpha z^*)\kappa,$$

whose solution, after replacing ω by $\theta_{-t}\omega$ and making t go to infinity, tends to zero provided $\bar{D} > m$, thus the internal structure of the attractor in this case consists of singleton subsets $A(\omega) = (s_{in}D\rho^*(\omega), 0)$ which means that there is not persistence of the microorganism.

□

We would like to remark that it is not possible to ensure the persistence of the microorganism in case $\bar{D} \leq m$ by using mathematical arguments even though our simulations show that the random attractor in this case is totally contained in $\mathscr{X}$, in other words, our model seems to guarantee the persistence of the microorganism.

3.1.4 Random pullback attractor for the stochastic system

We have proved that the system (3.7)-(3.8) has a unique global solution $u(t;0,\omega,u_0)$ which remains in $\mathscr{X}$, the first quadrant, for any $u_0 \in \mathscr{X}$ and generates a random dynamical system $\{\varphi_u(t,\omega)\}_{t\geq 0,\omega\in\Omega}$.

Now, we define a mapping

$$\mathscr{T} : \Omega \times \mathscr{X} \longrightarrow \mathscr{X}$$

as follows

$$\mathscr{T}(\omega,\zeta) = \left(\zeta_1 e^{\alpha z^*(\omega)}, \zeta_2 e^{\alpha z^*(\omega)}\right),$$

whose inverse is given by

$$\mathscr{T}^{-1}(\omega,\zeta) = \left(\zeta_1 e^{-\alpha z^*(\omega)}, \zeta_2 e^{-\alpha z^*(\omega)}\right).$$

We know that $v(t) = (s(t), x(t))$ and $u(t) = (\sigma(t), \kappa(t))$ are related by (3.6). Since $\mathscr{T}$ is a homeomorphism, thanks to Lemma B.0.1 in Appendix B we obtain a conjugated random dynamical system given by

$$\begin{aligned}\varphi_v(t,\omega)v_0 :=& \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)\mathscr{T}(\omega, v_0))\\ =& \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)u_0)\\ =& \mathscr{T}^{-1}(\theta_t\omega, u(t;\omega,u_0))\\ =& v(t;\omega,v_0),\end{aligned}$$

which means that $\{\varphi_v(t,\omega)\}_{t\geq 0,\omega\in\Omega}$ is a random dynamical system for our original stochastic system (3.3)-(3.4).

Moreover, thanks to Lemma B.0.2 in Appendix B, the random pullback attractor of the random system without taking into account the wall growth (3.7)-(3.8), $\mathscr{A} = \{A(\omega)\}_{\omega\in\Omega} \subset B_0(\omega)$, becomes into $\mathscr{A}^{\mathscr{T}} =$

$\{A^{\mathcal{T}}(\omega)\}_{\omega\in\Omega} \subset B_0^{\mathcal{T}}(\omega)$, the random pullback attractor of the system (3.3)-(3.4), where

$$B_0^{\mathcal{T}}(\omega) := \left\{(s,x) \in \mathcal{X} : s + x = Ds_{in}\rho^*(\omega)e^{-\alpha z^*(\omega)}\right\}.$$

In other words, each component of our random pullback attractor, $A^{\mathcal{T}}(\omega)$, can be written as

$$A^{\mathcal{T}}(\omega) := \left(s_{in}D\rho^*(\omega) - se^{-\alpha z^*(\omega)}, se^{-\alpha z^*(\omega)}\right).$$

In addition, we know that the internal structure of the attractor consists of singleton subsets $A^{\mathcal{T}}(\omega) = \left(s_{in}D\rho^*(\omega)e^{-\alpha z^*(\omega)}, 0\right)$ as long as $\bar{D} > m$. Apart from that, it is not possible to ensure the persistence of the microorganism otherwise even though our simulations show the persistence for several values of the parameters (see Section 3.1.5).

3.1.5 Numerical simulations and final comments

In this section we will show some numerical simulations concerning the results provided through the first part of this chapter by using the Euler-Maruyama's method already described in Chapter 1. In addition, in each figure the blue dashed lines represent the solution of the deterministic chemostat model (3.1)-(3.2) whereas the rest represent different realizations of the stochastic chemostat (3.3)-(3.4).

Henceforth, we consider $s_{in} = 1$, $a = 0.6$, $m = 3$ and we take $s_0 = 2.5$ and $x_0 = 5$ as initial pair. In addition, we specify the value of both the dilution rate and also the intensity of the noise which will help us to obtain different situations showing either the extinction or the persistence of the species, depending on the conditions previously given from the mathematical study.

On the one hand, in Figure 3.1 we consider $D = 3$ and we take $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right). It is easy to notice that the species become extinct in both cases, which is not surprising since condition (3.13) in Proposition 3.1.2 is fulfilled. Apart from that, the difference between both pictures can be noticed due to the effects caused by a larger quantity of noise in the second one.

Environmental effects by means of the white noise

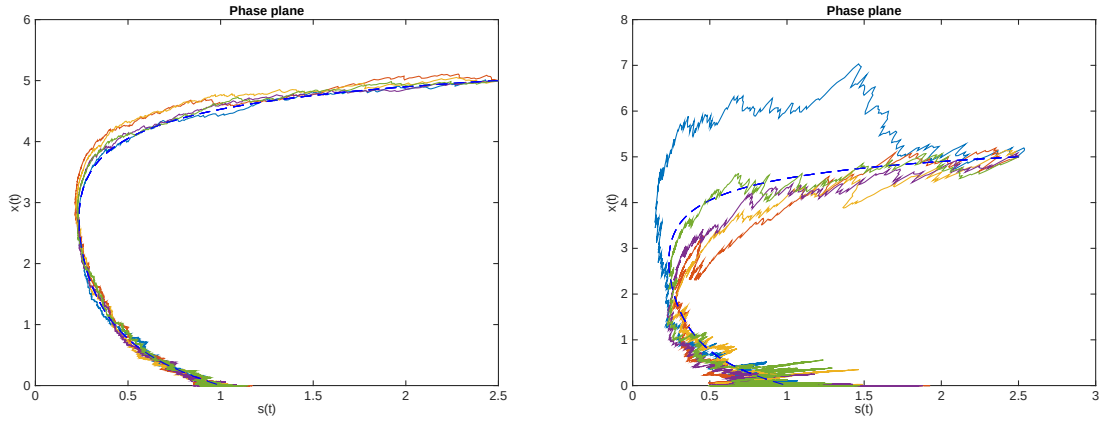


Figure 3.1: Extinction. $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right)

Now, in Figure 3.2 we increase the intensity of the noise to $\alpha = 1$ (left) and $\alpha = 1.5$ (right). In this case, since condition (3.13) in Proposition 3.1.2 is also true, the species become extinct in both cases and the effect of the different values of the quantify of noise can be also easily noticed.

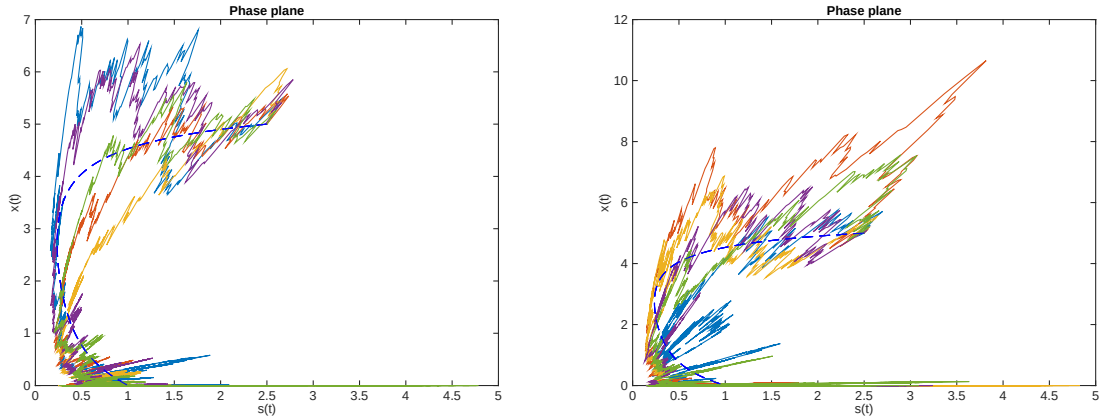


Figure 3.2: Extinction. $\alpha = 1$ (left) and $\alpha = 1.5$ (right)

On the other hand, in Figure 3.3 we consider $D = 1$ and we take $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right). In this case, condition (3.13) in Proposition 3.1.2 does not hold true, in fact, the persistence of the microbial biomass is obtained for the previous values of the parameters.

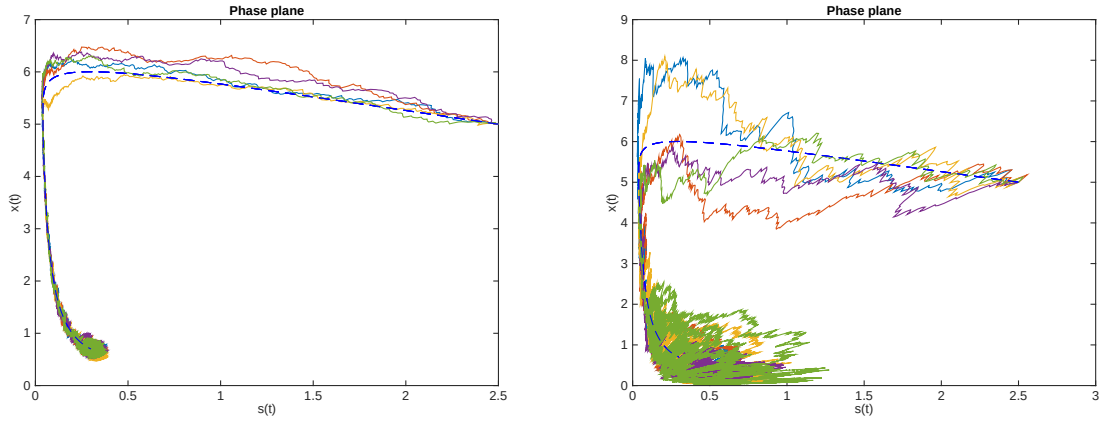


Figure 3.3: Persistence. $\alpha = 0.1$ (left) and $\alpha = 0.5$ (right)

Finally, in Figure 3.4 we consider $D = 1$ again and we increase the intensity of the noise to $\alpha = 1$ (left) and $\alpha = 1.5$ (right). In this case condition (3.13) in Proposition 3.1.2 is not fulfilled but, as explained when making the mathematical analysis, it is not possible to guarantee the persistence of the microorganisms, specially if the quantity of noise is considerable large.

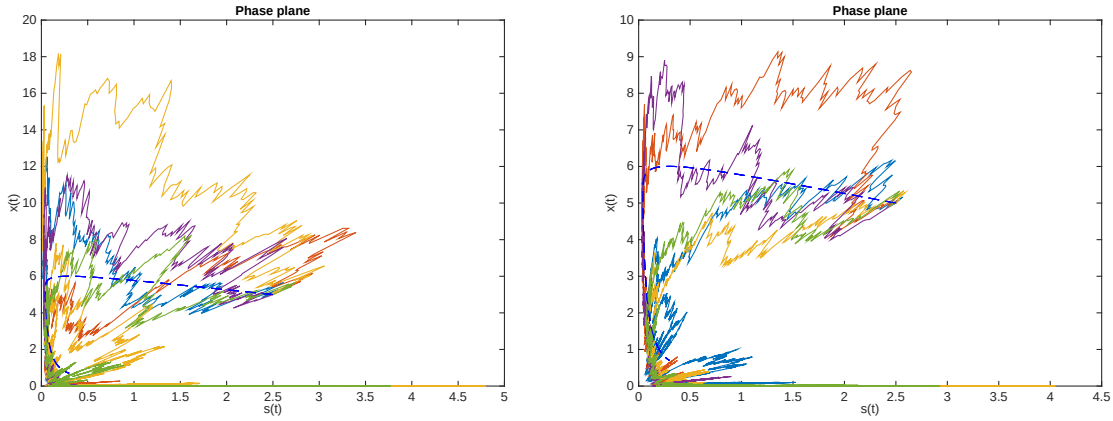


Figure 3.4: Extinction. $\alpha = 1$ (left) and $\alpha = 1.5$ (right)

We would like to emphasize the important differences when comparing the previous numerical simulations shown in this section with the ones presented in Chapter 1. In this case every realization of the solution of the stochastic chemostat model remains positive, as proved from the mathematical point of view in Theorem 3.1.1, independently of the initial values and, what is more, the intensity of the noise. It is mainly due to the way of modeling the stochasticity now and it is also a clear proof that this way is much more realistic from the biological point of view than the one used in Chapter 1.

3.2 Stochastic chemostat model with wall growth

In this section we analyze the equivalent model with wall growth. Then, let us now introduce the simplest chemostat model with wall growth

$$\frac{ds}{dt} = D(s_{in}-s) - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + b\nu x_1, \tag{3.14}$$

$$\frac{dx_1}{dt} = -(\nu+D)x_1 + c\frac{s}{a+s}x_1 - r_1x_1 + r_2x_2, \tag{3.15}$$

$$\frac{dx_2}{dt} = -\nu x_2 + c\frac{s}{a+s}x_2 + r_1x_1 - r_2x_2, \tag{3.16}$$

where $s(t)$, $x_1(t)$ and $x_2(t)$ denote concentrations of the nutrient and the two different microorganisms, respectively; $b \in (0,1)$ describes the fraction of dead biomass which is recycled, $\nu > 0$ is the collective death rate coefficient, $r_1 > 0$ and $r_2 > 0$ represent the rates at which the species stick on to and shear off from the walls, respectively, and $0 < c \leq m$ is the growth rate coefficient of the consumer species.

By introducing again a white noise in each equation of (3.14)-(3.16) and using the conversion between Itō and Stratonovich interpretations, we finally obtain the following stochastic system with wall growth

$$ds = \left[-\bar{D}s + b\nu x_1 - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + Ds_{in}\right]dt - \alpha s \circ dW(t), \tag{3.17}$$

$$dx_1 = \left[-\left(\nu+\bar{D}+r_1\right)x_1 + c\frac{s}{a+s}x_1 + r_2x_2\right]dt - \alpha x_1 \circ dW(t), \tag{3.18}$$

$$dx_2 = \left[r_1x_1 - \left(\nu + r_2 + \frac{\alpha^2}{2}\right)x_2 + c\frac{s}{a+s}x_2\right]dt - \alpha x_2 \circ dW(t). \tag{3.19}$$

3.2.1 Stochastic chemostat becomes a random chemostat

In this section we will analyze the stochastic chemostat model with wall growth (3.17)-(3.19) by performing a variable change which involves, as in the previous section, the well-known stationary Ornstein-Uhlenbeck process z^*. To this end, we will firstly define the new variables σ, κ_1 and κ_2 as follows

$$\sigma(t) = s(t)e^{\alpha z^*(\theta_t\omega)}, \quad \kappa_1(t) = x_1(t)e^{\alpha z^*(\theta_t\omega)} \quad \text{and} \quad \kappa_2(t) = x_2(t)e^{\alpha z^*(\theta_t\omega)}. \tag{3.20}$$

We will write z^* instead of $z^*(\theta_t\omega)$ and σ, κ_1 and κ_2 in place of $\sigma(t)$, $\kappa_1(t)$ and $\kappa_2(t)$.

From (3.17)-(3.19), by differentiation, we obtain the following random system with wall growth

$$\frac{d\sigma}{dt} = -(\bar{D}+\alpha z^*)\sigma + b\nu\kappa_1 - \frac{m\sigma e^{-\alpha z^*}}{a+\sigma e^{-\alpha z^*}}(\kappa_1+\kappa_2) + Ds_{in}e^{\alpha z^*}, \tag{3.21}$$

$$\frac{d\kappa_1}{dt} = -(\nu + \bar{D} + r_1 + \alpha z^*)\kappa_1 + c\frac{\sigma e^{-\alpha z^*}}{a + \sigma e^{-\alpha z^*}}\kappa_1 + r_2\kappa_2, \tag{3.22}$$

$$\frac{d\kappa_2}{dt} = r_1\kappa_1 - \left(\nu + r_2 + \frac{\alpha^2}{2} + \alpha z^*\right)\kappa_2 + c\frac{\sigma e^{-\alpha z^*}}{a + \sigma e^{-\alpha z^*}}\kappa_2. \tag{3.23}$$

3.2.2 Random chemostat generates a random dynamical system

In this section we prove that the random chemostat with wall growth (3.21)-(3.23) possesses a unique global solution which, moreover, generates a random dynamical system. In the sequel, we will denote $\mathscr{X} := \{(x, y, z) \in \mathbb{R}^3 : x \geq 0,\ y \geq 0,\ z \geq 0\}$, the first octant.

Theorem 3.2.1 *For any $\omega \in \Omega$ and any initial value $u_0 := (\sigma_0, \kappa_{10}, \kappa_{20}) \in \mathscr{X}$, where σ_0, κ_0, κ_{10} and κ_{20} denote $\sigma(0; 0, \omega, u_0)$, $\kappa(0; 0, \omega, u_0)$, $\kappa_1(0; 0, \omega, u_0)$ and $\kappa_2(0; 0, \omega, u_0)$, respectively, the random system* (3.21)-(3.23) *possesses a unique global solution*

$$u(\cdot; 0, \omega, u_0) := (\sigma(\cdot; 0, \omega, u_0), \kappa_1(\cdot; 0, \omega, u_0), \kappa_2(\cdot; 0, \omega, u_0)) \in \mathscr{C}^1([0, +\infty), \mathscr{X})$$

with $u(0; 0, \omega, u_0) = u_0$. In addition, the solution mapping generates a random dynamical $\varphi_u : \mathbb{R}^+ \times \Omega \times \mathscr{X} \to \mathscr{X}$ defined as

$$\varphi_u(t, \omega)u_0 = u(t; 0, \omega, u_0), \quad \text{for all } t \in \mathbb{R}^+,\ u_0 \in \mathscr{X},\ \omega \in \Omega,$$

the value at time t of the solution of system (3.21)-(3.23) *with initial state u_0 at time zero.*

Proof. Similarly to the proof of Theorem 3.1.1 and denoting

$$u(\cdot; 0, \omega, u_0) := (\sigma(\cdot; 0, \omega, u_0), \kappa_1(\cdot; 0, \omega, u_0), \kappa_2(\cdot; 0, \omega, u_0)),$$

system (3.21)-(3.23) can be written as

$$\frac{du}{dt} = L(\theta_t\omega)\ u + F(u, \theta_t\omega),$$

where

$$L(\theta_t\omega) = \begin{pmatrix} -(\bar{D} + \alpha z^*) & b\nu - m & -m \\ 0 & -(\nu + \bar{D} + r_1 + \alpha z^*) + c & r_2 \\ 0 & r_1 & -\left(\nu + r_2 + \frac{\alpha^2}{2} + \alpha z^*\right) + c \end{pmatrix}$$

and $F : \mathscr{X} \times \Omega \longrightarrow \mathbb{R}^3$ is given by

$$F(\eta, \theta_t\omega) = \begin{pmatrix} Ds_{in}e^{\alpha z^*} + \dfrac{ma}{a + \eta_1 e^{-\alpha z^*}}(\eta_2 + \eta_3) \\ \dfrac{-ca}{a + \eta_1 e^{-\alpha z^*}}\eta_2 \\ \dfrac{-ca}{a + \eta_1 e^{-\alpha z^*}}\eta_3 \end{pmatrix},$$

where $\eta = (\eta_1, \eta_2, \eta_3) \in \mathscr{X}$.

Since $t \mapsto z^*(\theta_t\omega)$ is continuous, L generates an evolution system on $\mathbb{R}^3$. In addition, $F(\cdot, \theta_t\omega) \in \mathscr{C}(\mathscr{X} \times [0, +\infty); \mathbb{R}^3)$ and is continuously differentiable with respect to the variables (η_1, η_2, η_3), whence it is locally Lipschitz with respect to $(\eta_1, \eta_2, \eta_3) \in \mathscr{X}$.

Therefore, thanks to classical results from the theory of ordinary differential equations, system (3.21)-(3.23) possesses a unique local solution. Let us check now that, in fact, this solution is a global one. In order to do that, we define $q(t) := \sigma(t) + \kappa_1(t) + \kappa_2(t)$, which satisfies the following differential equation

$$\frac{dq}{dt} \leq -\left(\frac{\alpha^2}{2} + \alpha z^*\right) q + Ds_{in} e^{\alpha z^*}, \tag{3.24}$$

since $c \leq m$ and $b < 1$. By solving (3.24), we obtain

$$q(t; 0, \omega, q_0) \leq q_0 e^{\frac{-\alpha^2}{2}t - \alpha \int_0^t z^* ds} + Ds_{in} \int_0^t e^{\alpha z^*} e^{\frac{\alpha^2}{2}s + \alpha \int_0^s z^* dr} e^{-\frac{\alpha^2}{2}t - \alpha \int_0^t z^* dr} ds, \tag{3.25}$$

thus q is clearly bounded by above by an expression which does not blow up at any finite time.

Furthermore, we have the following differential inequatily

$$\frac{dq}{dt} \geq -(\bar{D} + \alpha z^* + m + \nu) q + Ds_{in} e^{\alpha z^*},$$

therefore we obtain the following bound, which will be further very useful

$$\begin{aligned} q(t; 0, \omega, q_0) \geq & q_0 e^{-(\bar{D}+m+\nu)t - \alpha \int_0^t z^* ds} \\ & + Ds_{in} \int_0^t e^{\alpha z^*} e^{(\bar{D}+m+\nu)s + \alpha \int_0^s z^* dr} e^{-(\bar{D}+m+\nu)t - \alpha \int_0^t z^* dr} ds. \end{aligned} \tag{3.26}$$

It is straightforward to verify, similarly to the case without taking into account the wall growth, that the global solution of the random system (3.21)-(3.23) belongs to the first octant for any initial data $u_0 \in \mathscr{X}$ and $t \geq 0$. To this end, we will consider $\kappa_1 \geq 0$ and $\kappa_2 \geq 0$ and we will evaluate the equation (3.21) when $\sigma = 0$ such that we obtain

$$\left.\frac{d\sigma}{dt}\right|_{\sigma=0} = b\nu\kappa_1 + Ds_{in} e^{\alpha z^*} > 0.$$

Moreover, by taking $\sigma \geq 0$ and $\kappa_2 \geq 0$ and evaluating the equation (3.22) when $\kappa_1 = 0$, we have

$$\left.\frac{d\kappa_1}{dt}\right|_{\kappa_1=0} = r_2\kappa_2 > 0.$$

Finally, by taking $\sigma \geq 0$ and $\kappa_1 \geq 0$ and evaluating the equation (3.23) when $\kappa_2 = 0$, we obtain

$$\left.\frac{d\kappa_2}{dt}\right|_{\kappa_2=0} = r_1\kappa_1 > 0.$$

As a consequence, the unique global solution of the random system (3.21)-(3.23) remains in the first octant for any initial value $u_0 \in \mathscr{X}$.

Now we can define the mapping $\varphi_u : \mathbb{R}^+ \times \Omega \times \mathscr{X} \to \mathscr{X}$ given by

$$\varphi_u(t,\omega)u_0 := u(t;0,\omega,u_0), \quad \text{for all } t \geq 0,\ u_0 \in \mathscr{X},\ \omega \in \Omega.$$

Analogously to the case without wall growth, we obtain that the previous mapping is $(\mathscr{B}[0,\infty) \times \mathscr{F} \times \mathscr{B}(\mathscr{X}), \mathscr{B}(\mathscr{X}))-$measurable . Hence, $\{\varphi_u(t,\omega)\}_{t\geq 0,\omega\in\Omega}$ is a random dynamical system.

□

3.2.3 Existence of the random pullback attractor

In this section we study the existence and uniqueness of a random pullback attractor associated to the random chemostat model with wall growth (3.21)-(3.23), describing it explicitly whenever it is posible.

Proposition 3.2.1 *For any $\varepsilon > 0$, there exists a tempered compact random absorbing set $\widehat{B}_\varepsilon(\omega) \in \mathscr{E}(\mathscr{X})$ of the random dynamical system $\{\varphi_u(t,\omega)\}_{t\geq 0,\omega\in\Omega}$.*

Proof. Remember that $q = \sigma + \kappa_1 + \kappa_2$. Then, by replacing ω by $\theta_{-t}\omega$ in (3.25), we have

$$\begin{aligned} q(t;0,\theta_{-t}\omega,q_0) \quad &\leq \quad q_0 e^{-\frac{\alpha^2}{2}t-\alpha\int_{-t}^0 z^*(\theta_r\omega)dr} \\ &\quad + Ds_{in}\int_0^t e^{-\tau\left[\frac{\alpha^2}{2}-\frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau}+\frac{\alpha}{\tau}\int_{-\tau}^0 z^*(\theta_r\omega)dr\right]}d\tau, \end{aligned}$$

which tends to $Ds_{in}\rho_u^*(\omega)$ when t goes to infinity, where

$$\rho_u^*(\omega) := \int_0^\infty e^{-\tau\left[\frac{\alpha^2}{2}-\frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau}+\frac{\alpha}{\tau}\int_{-\tau}^0 z^*(\theta_r\omega)dr\right]}d\tau.$$

Now, after replacing ω by $\theta_{-t}\omega$ in (3.26), we obtain

$$\begin{aligned} q(t;0,\theta_{-t}\omega,q_0) \quad &\geq \quad q_0 e^{-(\tilde{D}+m+\nu)t-\alpha\int_{-t}^0 z^*(\theta_r\omega)dr} \\ &\quad + Ds_{in}\int_0^t e^{-\tau\left[(\tilde{D}+m+\nu)-\frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau}+\frac{\alpha}{\tau}\int_{-\tau}^0 z^*(\theta_r\omega)dr\right]}d\tau. \end{aligned}$$

The first term on the right hand in the last inequality tends to zero since $\bar{D}+m+\nu>0$. The second one tends to $Ds_{in}\rho_l^*(\omega)$, where

$$\rho_l^*(\omega):=\int_0^\infty e^{-\tau\left[(\bar{D}+m+\nu)-\frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau}+\frac{\alpha}{\tau}\int_{-\tau}^0 z^*(\theta_r\omega)dr\right]}d\tau.$$

We would like to note that the integrands defining $\rho_u^*(\omega)$ and $\rho_l^*(\omega)$ converge to zero when τ goes to infinity, but not the integrals. Moreover, $\rho_u^*(\omega)$ and $\rho_l^*(\omega)$ have sub-exponential growth.

Therefore, for every given $\varepsilon>0$ and any initial value $u_0\in E(\theta_{-t}\omega)$, there exists $T_E(\omega,\varepsilon)>0$ such that

$$-\varepsilon+Ds_{in}\rho_l^*(\omega)\le q(t;0,\theta_{-t}\omega,q_0)\le Ds_{in}\rho_u^*(\omega)+\varepsilon$$

for all $t\ge T_E(\omega,\varepsilon)$.

Now, we define

$$\widehat{B}_\varepsilon(\omega):=\left\{(\sigma,\kappa_1,\kappa_2)\in\mathscr{X}:-\varepsilon+Ds_{in}\rho_l^*(\omega)\le\sigma+\kappa_1+\kappa_2\le Ds_{in}\rho_u^*(\omega)+\varepsilon\right\},$$

thus $\widehat{B}_\varepsilon(\omega)\in\mathscr{E}(\omega)$ is a tempered compact random absorbing set in $\mathscr{X}$.

□

Hence, it follows directly from Proposition B.0.1 in Appendix B that the random dynamical system generated by the random system (3.21)-(3.23) possesses a unique random pullback attractor given by $\widehat{\mathscr{A}}=\{\widehat{A}(\omega)\}_{\omega\in\Omega}\subset\widehat{B}_\varepsilon(\omega)$, for all $\varepsilon>0$. Thus, $\widehat{\mathscr{A}}=\{\widehat{A}(\omega)\}_{\omega\in\Omega}\subset\widehat{B}_0(\omega)$.

Now we will investigate the random differential system (3.21)-(3.23) in more detail to obtain information concerning the internal structure of the corresponding random pullback attractor. To this end, we define the new variables

$$\kappa(t)=\kappa_1(t)+\kappa_2(t)\qquad\text{and}\qquad\xi(t)=\frac{\kappa_1(t)}{\kappa_1(t)+\kappa_2(t)}=\frac{x_1(t)}{x_1(t)+x_2(t)}\tag{3.27}$$

in order to transform our random system (3.21)-(3.23) into another system which will be more useful to understand the dynamics of the model. For the sake of simplicity we will write κ and ξ instead of $\kappa(t)$ and $\xi(t)$, as made previously.

Taking into account (3.27), the random system (3.21)-(3.23) becomes into the following random one

$$\frac{d\sigma}{dt}=-(\bar{D}+\alpha z^*)\sigma+b\nu\xi\kappa-\frac{m\sigma e^{-\alpha z^*}}{a+\sigma e^{-\alpha z^*}}\kappa+Ds_{in}e^{\alpha z^*},\tag{3.28}$$

$$\frac{d\kappa}{dt}=-\left(\nu+\alpha z^*+\frac{\alpha^2}{2}\right)\kappa+c\frac{\sigma e^{-\alpha z^*}}{a+\sigma e^{-\alpha z^*}}\kappa-D\xi\kappa,\tag{3.29}$$

$$\frac{d\xi}{dt} = -D\xi(1-\xi) - r_1\xi + r_2(1-\xi). \tag{3.30}$$

We will firstly study the Riccati equation (3.30) held by $\xi(t)$ since its dynamics is uncoupled with the rest of the system.

Defining the function $F_\xi : [0,\infty) \times [0,1] \longrightarrow \mathbb{R}$ as

$$F_\xi(t,\xi) = -D\xi(1-\xi) - r_1\xi + r_2(1-\xi) = -D\xi + D\xi^2 - r_1\xi + r_2 - r_2\xi,$$

it is straightforward to check that F_ξ is continuous (since it is a polynomial function) and locally Lipschitz respect to ξ, hence there exists a unique local solution of (3.30) which can be extended to a global one since ξ is bounded.

Moreover, by solving explicitly (3.30) we obtain

$$\xi(t;0,\omega,\xi_0) := \xi^* + \frac{1}{\left[\frac{1}{\xi_0-\xi^*} + \frac{D}{D+r_1+r_2-2D\xi^*}\right] e^{(D+r_1+r_2-2D\xi^*)t} - \frac{D}{D+r_1+r_2-2D\xi^*}}, \tag{3.31}$$

where

$$\xi^* := \frac{D+r_1+r_2-\sqrt{(D+r_1+r_2)^2-4Dr_2}}{2D}, \tag{3.32}$$

so that $D + r_1 + r_2 - 2D\xi^* > 0$.

By replacing now ω by $\theta_{-t}\omega$ in (3.31), we have

$$\xi(t;0,\theta_{-t}\omega,\xi_0) = \xi^* + \frac{1}{\left[\frac{1}{\xi_0-\xi^*} + \frac{D}{D+r_1+r_2-2D\xi^*}\right] e^{(D+r_1+r_2-2D\xi^*)t} - \frac{D}{D+r_1+r_2-2D\xi^*}}.$$

Hence, since $D + r_1 + r_2 - 2D\xi^* > 0$, we obtain

$$\lim_{t\to+\infty} \xi(t;0,\theta_{-t}\omega,\xi_0) = \xi^*.$$

Now, we are interested in studying the random system

$$\frac{d\sigma}{dt} = -(\bar{D} + \alpha z^*)\sigma + bv\xi^*\kappa - \frac{m\sigma e^{-\alpha z^*}}{a+\sigma e^{-\alpha z^*}}\kappa + Ds_{in}e^{\alpha z^*}, \tag{3.33}$$

$$\frac{d\kappa}{dt} = -\left(v + \alpha z^* + \frac{\alpha^2}{2}\right)\kappa + c\frac{\sigma e^{-\alpha z^*}}{a+\sigma e^{-\alpha z^*}}\kappa - D\xi^*\kappa, \tag{3.34}$$

in order to obtain extra information about the internal structure of the random pullback attractor.

On the one hand, from (3.34) we obtain

$$\frac{d\kappa}{dt} \leq -\left(\nu + \alpha z^* + \frac{\alpha^2}{2} - c\right)\kappa$$

whose solution is given by

$$\kappa(t;0,\omega,\kappa_0) \leq \kappa_0 e^{-\left(\nu+\frac{\alpha^2}{2}-c\right)t-\alpha\int_0^t z^* ds}. \tag{3.35}$$

Now, after replacing ω by $\theta_{-t}\omega$ in (3.35), we know that

$$\lim_{t\to+\infty} \kappa(t;0,\theta_{-t}\omega,\kappa_0) \leq \varepsilon,$$

for any $\varepsilon > 0$, provided

$$\nu + \frac{\alpha^2}{2} > c. \tag{3.36}$$

On the contrary, as long as $\nu + \frac{\alpha^2}{2} < c$, (3.35) does not provide any extra information about the asymptotic dynamics of the microbial biomass.

On the other hand, from (3.29) we obtain the following inequalities

$$-\left(\nu + \frac{\alpha^2}{2} + D + \alpha z^*\right)\kappa \leq \frac{d\kappa}{dt} \leq -\left(\nu + \frac{\alpha^2}{2} - c + \alpha z^*\right)\kappa. \tag{3.37}$$

In addition, we can easily obtain the next lower bound from (3.28) for the equation describing the dynamics of the substrate

$$\frac{d\sigma}{dt} \geq -(\bar{D} + \alpha z^*)\sigma + (b\nu\xi^* - m)\kappa + Ds_{in}e^{\alpha z^*}, \tag{3.38}$$

where ξ^* is given by (3.32). By using now (3.37) we are able to solve (3.38) whichever the sign of $b\nu\xi^* - m$, so that we split our analysis into the following cases.

- **Case A:** If $b\nu\xi^* - m \geq 0$ holds, we have

  $$\lim_{t\to+\infty} \sigma(t;0,\theta_{-t}\omega,\sigma_0) \geq s_{in}D\rho_\sigma^*(\omega) - \varepsilon,$$

  for any $\varepsilon > 0$, where

  $$\rho_\sigma^*(\omega) := \int_0^\infty e^{-\tau\left[\bar{D} - \frac{\alpha z^*(\theta_{-\tau}\omega)}{\tau} + \frac{\alpha}{\tau}\int_{-\tau}^0 z^*(\theta_r\omega)dr\right]} d\tau.$$

  We note that $\rho_\sigma^*(\omega)$ is well-defined and has sub-exponential growth. Hence, we analyze the following cases

  - **Case A-1.** If $\nu + \frac{\alpha^2}{2} > c$, we obtain

    $$\lim_{t\to+\infty} \sigma(t;0,\theta_{-t}\omega,\sigma_0) \geq s_{in}D\rho_\sigma^*(\omega) - \varepsilon \quad \text{and} \quad \lim_{t\to+\infty} \kappa(t;0,\theta_{-t}\omega,\kappa_0) \leq \varepsilon$$

for any $\varepsilon > 0$. In this case, we obtain the following compact tempered random absorbing set for the system (σ, κ), which is given by

$$B_1(\omega) = \left\{(\sigma, 0) \in \mathscr{X} : s_{in} D\rho_\sigma^*(\omega) \leq \sigma \leq s_{in} D\rho_u^*(\omega)\right\},$$

which means that there is not persistence of the microorganisms since the absorbing set is reduced to a line which is totally contained inside the axis $\kappa = 0$.

- **Case A-2.** If $\nu + \frac{\alpha^2}{2} < c$, we obtain

$$\lim_{t \to +\infty} \sigma(t; 0, \theta_{-t}\omega, \sigma_0) \geq s_{in} D\rho_\sigma^*(\omega) - \varepsilon \quad \text{and} \quad \lim_{t \to +\infty} \kappa(t; 0, \theta_{-t}\omega, \kappa_0) \leq \varepsilon$$

for any $\varepsilon > 0$. In this case, we have the following tempered compact random absorbing set associated to the random system (σ, κ), which is given by

$$B_2(\omega) = \left\{(\sigma, \kappa) \in \mathscr{X} : \sigma + \kappa \leq s_{in} D\rho_u^*(\omega),\, \sigma \geq s_{in} D\rho_\sigma^*(\omega)\right\}.$$

In that case we are not able to establish conditions to ensure the persistence of both microorganisms. Nevertheless, the numerical simulations will show that we can obtain persistence in the current case for many different values of the parameters involved in the model.

- **Case B:** If $b\nu\xi^* - m < 0$ holds, we need to distinguish two cases again:

  - **Case B-1.** If $\nu + \frac{\alpha^*}{2} > c$, we have

$$\lim_{t \to +\infty} \sigma(t; 0, \theta_{-t}\omega, \sigma_0) \geq s_{in} D\rho_\sigma^*(\omega) - \varepsilon \quad \text{and} \quad \lim_{t \to +\infty} \kappa(t; 0, \theta_{-t}\omega, \kappa_0) \leq \varepsilon$$

  for any $\varepsilon > 0$. In this case, $B_1(\omega)$ is again a tempered compact random absorbing set for the random system (σ, κ). It means that both microorganisms, the ones in the medium and also the ones sticked on the walls of the culture vessel, will become extinct.

  - **Case B-2.** If $\nu + \frac{\alpha^2}{2} < c$, we have

$$\lim_{t \to +\infty} \sigma(t; 0, \theta_{-t}\omega, \sigma_0) \geq -\infty \quad \text{and} \quad \lim_{t \to +\infty} \kappa(t; 0, \theta_{-t}\omega, \kappa_0) \leq \infty.$$

  In this case it is not possible to get extra information from the dynamics of the nutrient and the species. As a result, $\widehat{B}_0(\omega)$ is a compact tempered compact random absorbing set for the random system (σ, κ). We would also like to remark that it is not possible to guarantee the persistence of the microorganisms even though the numerical simulations show the persistence for many values of the parameters, as shown in Section 3.2.5.

Finally, we state Table 3.1 to summarize the results of the previous study.

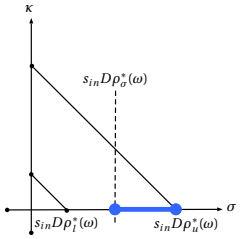
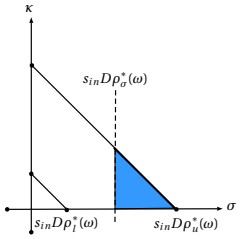
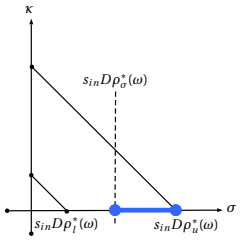
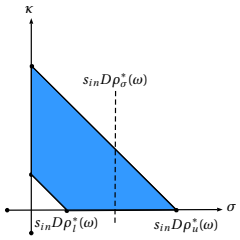
		ASYMPTOTIC BOUNDS	ABSORBING SET SYSTEM (3.33)-(3.34)
Case A: $b\nu\xi^* - m \geq 0$	(A-1) $\nu + \frac{\alpha^2}{2} > c$	$\lim_{t\to+\infty} \sigma(t) \geq s_{in} D\rho_\sigma^*(\omega) - \varepsilon$	
		$\lim_{t\to+\infty} \kappa(t) \leq \varepsilon$	
	(A-2) $\nu + \frac{\alpha^2}{2} < c$	$\lim_{t\to+\infty} \sigma(t) \geq s_{in} D\rho_\sigma^*(\omega) - \varepsilon$	
		$\kappa(t)$ does not provide any extra information	
Case B: $b\nu\xi^* - m < 0$	(B-1) $\nu + \frac{\alpha^2}{2} > c$	$\lim_{t\to+\infty} \sigma(t) \geq s_{in} D\rho_\sigma^*(\omega) - \varepsilon$	
		$\lim_{t\to+\infty} \kappa(t) \leq \varepsilon$	
	(B-2) $\nu + \frac{\alpha^2}{2} < c$	$\sigma(t)$ does not provide any extra information	
		$\kappa(t)$ does not provide any extra information	

Table 3.1: Absorbing sets for the random system (3.33)-(3.34)

3.2.4 Random pullback attractor for the stochastic chemostat

In this section, we define a random dynamical system associated to the original stochastic chemostat model with wall growth by using the conjugation Lemma B.0.1 in Appendix B. In addition, we will provide information about the pullback random attractor associated to the original stochastic system as well as its internal structure.

Hence, we define a mapping

$$\mathscr{T} : \Omega \times \mathscr{X} \longrightarrow \mathscr{X},$$

similarly to the one in Section 3.1, as follows

$$\mathscr{T}(\omega,\zeta) = \left(\zeta_1 e^{\alpha z^*(\omega)}, \zeta_2 e^{\alpha z^*(\omega)}, \zeta_3 e^{\alpha z^*(\omega)}\right),$$

whose inverse is given by

$$\mathscr{T}^{-1}(\omega,\zeta) = \left(\zeta_1 e^{-\alpha z^*(\omega)}, \zeta_2 e^{-\alpha z^*(\omega)}, \zeta_3 e^{-\alpha z^*(\omega)}\right).$$

Since $v(t) = (s(t), x_1(t), x_2(t))$ and $u(t) = (\sigma(t), \kappa_1(t), \kappa_2(t))$ are both related by (3.20) and $\mathscr{T}$ is a homeomorphism, thanks to Lemma B.0.1 in Appendix B we obtain again a conjugated random dynamical system given by

$$\begin{aligned}
\varphi_v(t,\omega)v_0 :=& \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)\mathscr{T}(\omega, v_0)) \\
=& \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)u_0) \\
=& \mathscr{T}^{-1}(\theta_t\omega, u(t;\omega,u_0)) \\
=& v(t;\omega,v_0),
\end{aligned}$$

which means that $\{\varphi_v(t,\omega)\}_{t\geq 0,\omega\in\Omega}$ is a random dynamical system for our original stochastic system (3.17)-(3.19).

In addition, thanks to Lemma B.0.2 in Appendix B, the random pullback attractor of the random system with wall growth (3.21)-(3.23), $\widehat{\mathscr{A}} = \{\widehat{A}(\omega)\}_{\omega\in\Omega} \subset \widehat{B}_0(\omega)$, becomes now into $\widehat{\mathscr{A}^{\mathscr{T}}} = \{\widehat{A}^{\mathscr{T}}(\omega)\}_{\omega\in\Omega} \subset \widehat{B}_0^{\mathscr{T}}(\omega)$, the random pullback attractor associated to the original stochastic system with wall growth (3.17)-(3.19), where

$$\widehat{B}_0^{\mathscr{T}}(\omega) = \left\{(s,x_1,x_2) \in \mathscr{X} : Ds_{in}\rho_l^*(\omega)e^{-\alpha z^*(\omega)} \leq s + x_1 + x_2 \leq Ds_{in}\rho_u^*(\omega)e^{-\alpha z^*(\omega)}\right\}.$$

Table 3.2 in the next page shows information on the random pullback attractor $\widehat{\mathscr{A}^{\mathscr{T}}} = \{\widehat{A}^{\mathscr{T}}(\omega)\}_{\omega\in\Omega}$, taking into account the analysis carried out at the end of Section 3.2.3.

Environmental effects by means of the white noise

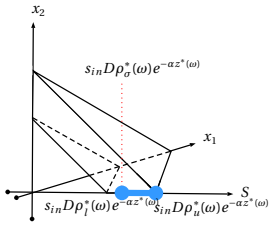
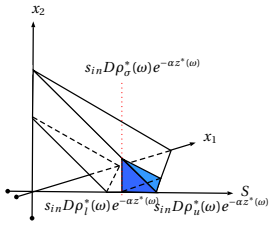
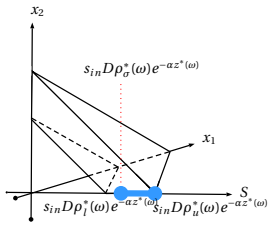
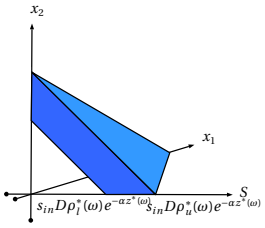
		ASYMPTOTIC BOUNDS	ATTRACTOR INTERNAL STRUCTURE
Case A: $bvc_\xi - m \geq 0$	(A-1) $\nu + \frac{\alpha^2}{2} > c$	$\lim_{t\to+\infty} S(t) \geq s_{in} D\rho^*_\sigma(\omega) e^{-\alpha z^*(\omega)} - \varepsilon$	
		$\lim_{t\to+\infty} [x_1(t) + x_2(t)] \leq \varepsilon$	
	(A-2) $\nu + \frac{\alpha^2}{2} < c$	$\lim_{t\to+\infty} S(t) \geq s_{in} D\rho^*_\sigma(\omega) e^{-\alpha z^*(\omega)} - \varepsilon$	
		$x_1 + x_2$ does not provide any extra information	
Case B: $bvc_\xi - m < 0$	(B-1) $\nu + \frac{\alpha^2}{2} > c$	$\lim_{t\to+\infty} S(t) \geq s_{in} D\rho^*_\sigma(\omega) e^{-\alpha z^*(\omega)} - \varepsilon$	
		$\lim_{t\to+\infty} [x_1(t) + x_2(t)] \leq \varepsilon$	
	(B-2) $\nu + \frac{\alpha^2}{2} < c$	S does not provide any extra information	
		$x_1 + x_2$ does not provide any extra information	

Table 3.2: Internal structure of the random attractor - Stochastic chemostat model with wall growth

3.2.5 Numerical simulations and final comments

In this section we show some numerical simulations concerning the stochastic chemostat model with wall growth (3.17)-(3.19) analyzed in Section 3.2. In each figure we display four different panels: there is a big one on the left showing the phase plane with the general dynamics of the nutrient and the microorganisms; on the other hand, three smaller panels can be seen on the right to show the dynamics of the substrate and the different species individually, depending on the time. In this way, we can easily observe the asymptotic behavior of every state variable involved in our chemostat. We also recall that the blue dashed lines represent the solution of the deterministic chemostat with wall growth (3.14)-(3.16) whereas the rest represent different realizations of the stochastic one given by (3.17)-(3.19). Moreover, the thick black asterisk denotes the initial value (s_0, x_{10}, x_{20}).

On the one hand, in Figure 3.5 we consider $s_{in} = 1$, $D = 2$, $a = 0.6$, $m = 5$, $b = 0.5$, $\nu = 2$, $c = 1.2$, $r_1 = 0.2$, $r_2 = 0.8$ and we take $s_0 = 5$, $x_{10} = 10$ and $x_{20} = 10$ as initial triple. In addition, we consider $\alpha = 0.1$ as intensity of the noise. As a result, we can observe that both species, the ones in the medium and also the ones sticked on the walls of the culture vessel, become extinct, which is not surprising due to the fact that condition (3.36) holds true.

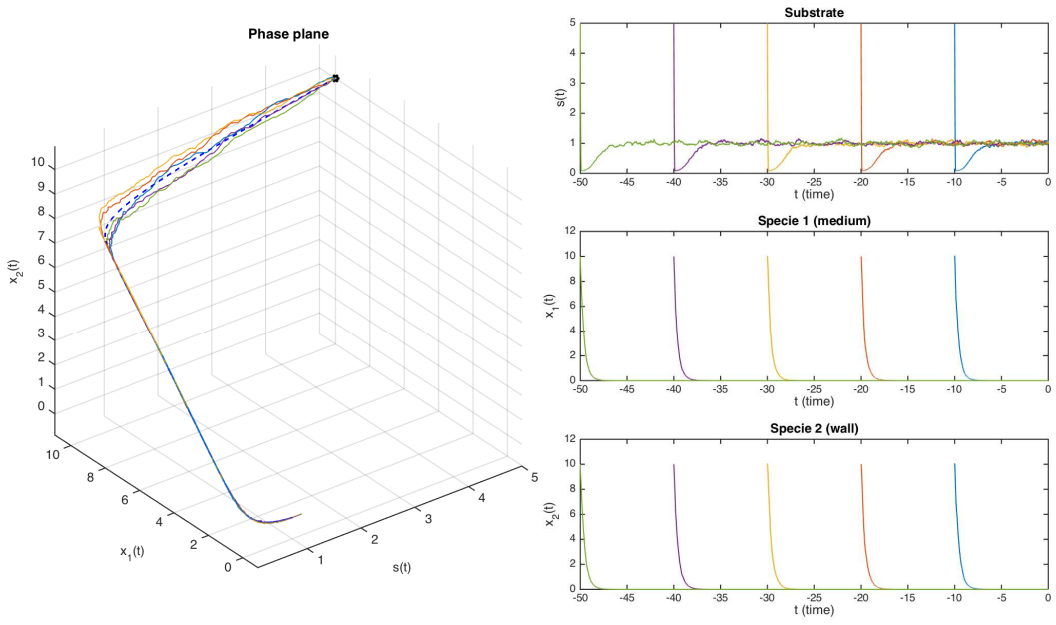


Figure 3.5: Extinction. $\alpha = 0.1$

In Figure 3.6 we increase the quantity of the noise to $\alpha = 0.5$. In this case condition (3.36) is also fulfilled, thus we obtain the extinction of the species.

Environmental effects by means of the white noise

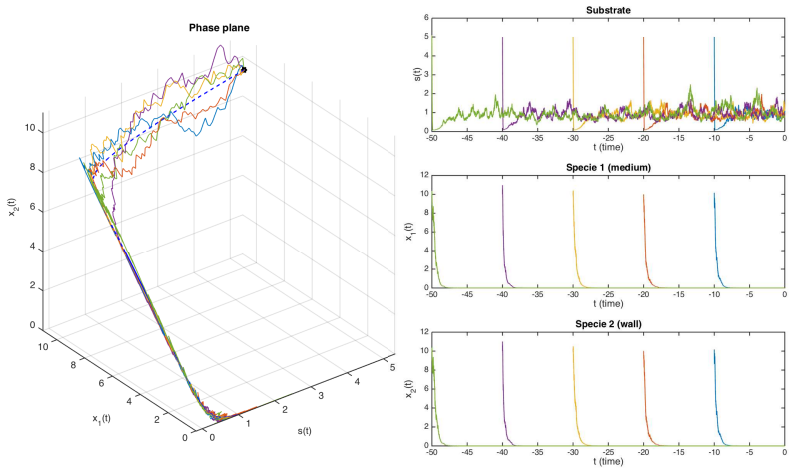


Figure 3.6: Extinction. $\alpha = 0.5$

On the other hand, in Figure 3.7 we consider $s_{in} = 1$, $D = 2$, $a = 0.6$, $m = 5$, $b = 0.5$, $\nu = 0.3$, $c = 3$, $r_1 = 0.2$, $r_2 = 0.8$, we take $s_0 = 5$, $x_{10} = 10$ and $x_{20} = 10$ as initial triple and we consider $\alpha = 0.1$. In this case condition (3.36) does not hold true, in fact, the microbial biomass persists even though it is not possible to ensure the persistence from the mathematical point of view.

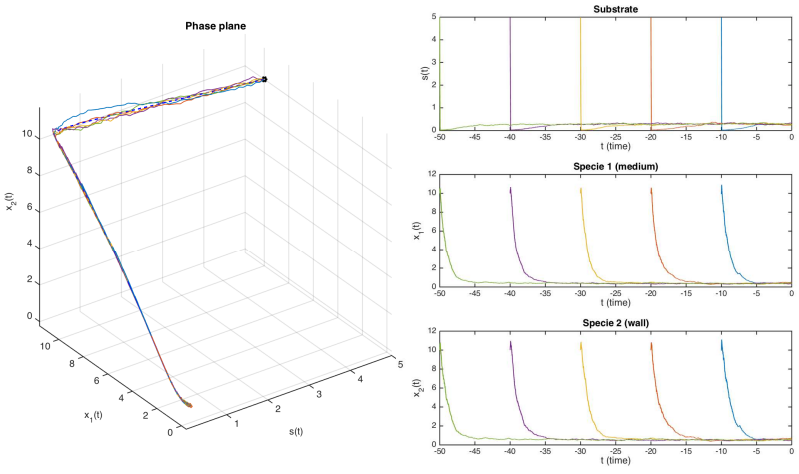


Figure 3.7: Persistence. $\alpha = 0.1$

Finally, in Figure 3.8 we increase the quantity of the noise to $\alpha = 0.5$. In this case, condition (3.36) is not fulfilled either but, although the persistence cannot be guaranteed as we previously deduced from the

mathematical study, both species, the ones in the medium and also the ones sticked on the walls of the culture vessel, persists, as can be easily observed in the last two panels. Apart from that, in this figure we can also notice the increment of the quantity of the noise when looking at the different realizations, which are more disturbed that the ones in the previous figure with $\alpha = 0.1$.

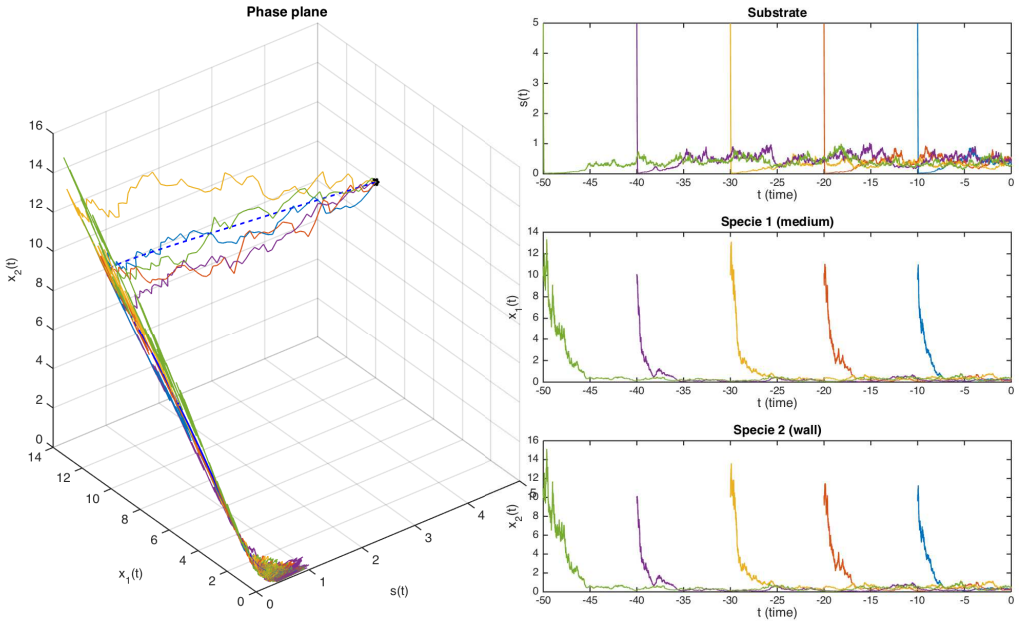


Figure 3.8: Persistence. $\alpha = 0.5$

We would like to highlight that every realization in each figure of this section remains positive for any initial value and every value of the parameters involved in the system, as proved in Theorem 3.2.1. In addition, it is not strange the fact of having extinction in Figures 3.5 and 3.6 whereas we obtain the persistence in Figures 3.7 and 3.8. The most important reason, apart from the intensity of the noise, is the value of the collective death coefficient which is much smaller in the last two figures and it directly has a huge influence on the condition (3.36), thanks to which the extinction can be (or not) ensured, independently of the other parameters.

CHAPTER 4

Modeling and analysis of environmental effects caused by the fractional Brownian motion in chemostat models

In this last chapter we analyze the chemostat model after introducing a stochastic perturbation given by means of a new kind of noise: the fractional Brownian motion B^H indexed by the Hurst parameter H. Firstly, we will introduce this new noise and we will mention its main properties. Since the fractional Brownian motion for $H \neq 1/2$ is not a semimartingale, we cannot use the Itō integral in this setting, hence we need to introduce a new integral against B^H. To be more precise, we define the stochastic integral by using fractional calculus tools, for what the main ingredient is the use of fractional derivatives. The main advantage of using this definition is that it is a pathwise integral and, therefore, it does not produce exceptional sets which are against the generation of a cocycle. Then, we will establish a result concerning the existence and uniqueness of a global solution of our stochastic system and will provide some conditions under which our system generates a semigroup operator, which allows us to define the solution in a mild sense. Since we do not transform the stochastic chemostat model perturbed by B^H into a random system (as we already did in the previous chapters when dealing with $B^{\frac{1}{2}}$), this means that the norm of the solution depends in particular of the norm of the noise, which prevents us to use a suitable version of Gronwall's lemma to conclude, for instance, the existence of an absorbing ball. This is the main reason for which we will introduce a sequence of stopping times, which will allow us to control the contribution of the noise, and, therefore, to ensure in particular the existence of a (discrete) tempered absorbing set which will be determinant to establish the existence and uniqueness of a (discrete) random pullback attractor. We would like to emphasize that, in a first step, we discretize the random dynamical system, in a way that we only consider it acting on the sequence of stopping times. Indeed, when we look at the cocycle mapping on the stopping times we can handle the estimates of the solution. In a second step, we will obtain the exis-

tence and uniqueness of the continuous random pullback attractor associated to the continuous random dynamical system, which rests upon the relationship between the discrete and continuous tempered sets and the properties of the stopping times. Finally, we will show some numerical simulations to observe the effects of the fractional Brownian motion in the chemostat models previously studied.

The results and explanations concerning this chapter can be found in [11].

4.1 Chemostat models and fractional noise

In this section we will consider the simplest deterministic chemostat model (3)-(4), which was already presented in the introductory chapter, and we will introduce stochasticity by using a different kind of noise which significantly differs from the standard Brownian motion used in Chapters 1 and 3. This new noise, that is becoming progressively more and more popular between researchers of several branches of scientific knowledge, is the fractional Brownian motion, fBm for short, that was introduced originally by Kolmogorov in 1940 (see [57]) to study the long term storage capacity of reservoirs along the Nile river. The fBm consists of a generalization of the standard Brownian motion, as we will see in Section 4.2. The main reason to introduce this new noise in our model is due to the fact that it has been proved to be a good candidate to model random long-time influences in climate systems, hydrology and medicine, to name a few applications.

Similarly to the way of modeling in Chapter 3, when using the standard Wiener process, we will introduce some disturbances in the deterministic model (3)-(4) by using the fBm such that we obtain the following stochastic differential system

$$ds = \left[(s_{in}-s)D - \frac{msx}{a+s}\right]dt + \alpha s dB^H(t), \tag{4.1}$$

$$dx = \left[-Dx + \frac{msx}{a+s}\right]dt + \alpha x dB^H(t), \tag{4.2}$$

where $B^H(\cdot)$ denotes the fBm with Hurst parameter $H \in (1/2, 1)$ and $\alpha > 0$ refers to the quantity of noise, $s(t)$ and $x(t)$ denote concentrations of the nutrient and the microbial biomass, respectively; s_{in} denotes the volumetric dilution rate, a is the half-saturation constant, D is the dilution rate and m is the maximal consumption rate of the nutrient and also the maximal specific growth rate of microorganisms. We notice that all parameters are positive and we use a function Holling type-II as functional response of the microorganism describing how the nutrient is consumed by the species.

Up to now, we have just mentioned the chemostat model without taking into account the wall growth. Of course that we can also consider the equivalent stochastic model with wall growth, which was already introduced in the introductory chapter, affected by an fBm as well, given by the following system of stochastic

differential equations

$$ds = \left[(s_{in}-s)D - \frac{ms}{a+s}x_1 - \frac{ms}{a+s}x_2 + bvx_1\right]dt + \alpha s dB^H(t), \tag{4.3}$$

$$dx_1 = \left[-(v+D)x_1 + \frac{cs}{a+s}x_1 - r_1x_1 + r_2x_2\right]dt + \alpha x_1 dB^H(t), \tag{4.4}$$

$$dx_2 = \left[-vx_2 + \frac{cs}{a+s}x_2 + r_1x_1 - r_2x_2\right]dt + \alpha x_2 dB^H(t), \tag{4.5}$$

where $B^H(\cdot)$ denotes again the fBm with Hurst parameter $H \in (1/2, 1)$ and the rest of parameters and functions have the same meaning than in system (6)-(8).

From now on, we will focus our study just on the simplest stochastic chemostat model (4.1)-(4.2) since the same analysis could be made for the model with wall growth (4.3)-(4.5).

4.2 The fractional Brownian motion and the fractional integral

The fractional Brownian motion is a centered Gaussian process $B^H = \{B^H(t)\}_{t\in\mathbb{R}}$ indexed by the Hurst parameter $H \in (0,1)$. In fact, it satisfies the long-memory property when $H > 1/2$. In addition, it is a self-similar stochastic process characterized by the stationarity of its increments. When $H = 1/2$, the fBm reduces to the standard Brownian motion. Moreover, it has continuous sample paths and its covariance function is given by

$$\mathbb{E}\left(B^H(s), B^H(t)\right) = \frac{1}{2}\left(t^{2H} + s^{2H} - |t-s|^{2H}\right).$$

Thanks to Kolmogorov's Theorem, there exists a continuous version of the fractional Brownian motion, whose canonical interpretation is as follows. Let $\Omega = \mathscr{C}_0(\mathbb{R},\mathbb{R})$ be the space of continuous functions on $\mathbb{R}$ with values in $\mathbb{R}$ which are zero at zero. This set is equipped with the compact open topology. We define $\mathscr{F}$ as the Borel $\sigma-$algebra and $\mathbb{P}$ is the probability measure, or probability distribution, of the fBm. Then, the quadruple $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$ is an ergodic metric dynamical system, where $\{\theta_t\}_{t\in\mathbb{R}}$ denotes the Wiener shift defined as in Appendix A. For more detailed information, see [39]. This canonical process has a version, which will be denoted by ω, which is $\beta-$Hölder continuous on any interval $[-k,k] \subset \mathbb{R}$ for $\beta < H$, see [58].

When $H \neq 1/2$, the fBm behaves in a very different way than the standard Brownian motion. In fact, B^H is neither a martingale nor a Markov process hence we cannot use the Itō's theory to define the stochastic integral with integrator the fBm. This has the disadvantage that we need to define a different integral with respect to B^H, but, as a positive counterpart, the so-called *pathwise integral* does not produce exceptional sets. Let us remind that, as far as the cocycle property is concerned, exceptional sets are not permitted. As it is well-known, the Itō's integral produces exceptional sets and this is the reason for which in all the previous chapters we always transformed the stochastic systems into random ones that were handled by deterministic techniques. In this chapter we will not use any transformation but instead we deal with the stochastic chemostat with fBm.

In the rest of the section, we will introduce some basic concepts concerning the theory of the fractional calculus which will involve two essential ingredients: the fractional derivatives and the fractional integral.

From now on, $T > 0$ will denote a positive real time. Then, we introduce the following usual Hölder spaces.

Definition 4.2.1 *Let $\beta > 0$ be a constant and $d \in \mathbb{N}$. Then, $\mathscr{C}^{\beta}([a,b];\mathbb{R}^d)$ denotes the space of Hölder continuous functions $f : [a,b] \longrightarrow \mathbb{R}^d$ with values in $\mathbb{R}^d$ equipped with the norm*

$$\begin{aligned} \|f\|_{\beta,a,b} &:= \|f\|_{\infty,a,b} + |||f|||_{\beta,a,b} \\ &= \sup_{t\in[a,b]} |f(t)| + \sup_{a\leq s<t\leq b} \frac{|f(t)-f(s)|}{(t-s)^{\beta}} < \infty. \end{aligned}$$

Moreover, we present now the damped Hölder spaces which are given as in the following definition.

Definition 4.2.2 *Let $\beta > 0$ be a constant and $d \in \mathbb{N}$. Then, $\mathscr{C}^{\beta}_{\beta}([a,b];\mathbb{R}^d)$ denotes the space of continuous functions $f : [a,b] \longrightarrow \mathbb{R}^d$ with values in $\mathbb{R}^d$ equipped with the norm*

$$\begin{aligned} \|f\|_{\beta,\beta,a,b} &:= \|f\|_{\infty,a,b} + |||f|||_{\beta,\beta,a,b} \\ &= \sup_{t\in[a,b]} |f(t)| + \sup_{a\leq s<t\leq b} (s-a)^{\beta} \frac{|f(t)-f(s)|}{(t-s)^{\beta}} < \infty. \end{aligned}$$

We would like to notice that the damped Hölder spaces defined in the previous definition are Banach spaces (see [21, 62]).

Now, we introduce the concept of fractional derivatives which will allow us to define the fractional integral. We refer every interested reader to [78] for more detailed information on fractional calculus.

Definition 4.2.3 *Let $\alpha \in (0,1)$ be a constant and $a < b$ real numbers. Then, the fractional derivatives of K and ω, respectively, are defined as follows*

$$\begin{aligned} D^{\alpha}_{a+}K(r) &:= \frac{1}{\Gamma(1-\alpha)}\left(\frac{K(r)}{(r-a)^{\alpha}} + \alpha\int_a^r \frac{K(r)-K(s)}{(r-s)^{\alpha+1}}ds\right), \\ D^{1-\alpha}_{b-}\omega_{b-}(r) &:= \frac{1}{\Gamma(\alpha)}\left(\frac{\omega(r)-\omega(b)}{(b-r)^{1-\alpha}} + (1-\alpha)\int_r^b \frac{\omega(r)-\omega(s)}{(s-r)^{2-\alpha}}ds\right), \end{aligned}$$

where Γ denotes the Gamma function.

It is straightforward to prove the following bound concerning the fractional derivative of the fractional Brownian motion.

Lemma 4.2.1 *For every $\beta \in (1/2, H)$ and $a, b, x \in \mathbb{R}$ such that $[a, b] \subseteq [0, T]$ and $x \in [a, b]$, for $\alpha > 1 - \beta$ the following inequality holds true*

$$|D_{b-}^{1-\alpha}\omega_{b-}(x)| \leq c(\beta)|||\omega|||_{\beta,0,T}(b-x)^{\beta+\alpha-1}.$$

Now, we introduce the fractional integral.

Definition 4.2.4 *Let $K \in \mathscr{C}_{\beta}^{\beta}([a, b]; \mathbb{R}^d)$ such that $\beta > 1/2$ and $1 - \beta < \alpha < \beta$. Then, we define the fractional integral of K with respect to the fBm as follows*

$$\int_a^b K(r)d\omega(r) := (-1)^{\alpha}\int_a^b D_{a+}^{\alpha}K(r)D_{b-}^{1-\alpha}\omega_{b-}(r)dr, \tag{4.6}$$

where the fractional derivatives inside the integral on the right hand side of (4.6) *are defined as in Definition 4.2.3.*

For a detailed construction of the pathwise stochastic integral (4.6) as well as its main properties, we refer the reader to [78]. In the following result, nevertheless, we collect some of these properties.

Lemma 4.2.2 *Given $T > 0$, $K \in \mathscr{C}_{\beta}^{\beta}([0, T]; \mathbb{R}^d)$, $\omega \in \Omega$ an fBm with $1 - \beta < \alpha < \beta$. Then,*

1) *For $[a, b] \subseteq [0, T]$, we have the following estimate of the fractional integral given by* (4.6)

$$\left|\int_a^b K(r)d\omega(r)\right| \leq c(\alpha, \beta)\|K\|_{\beta,\beta,0,T}|||\omega|||_{\beta,0,T}(b-a)^{\beta}. \tag{4.7}$$

2) *For $[a, b] \subseteq [0, T]$ and $p \in \mathbb{R}$ such that $[a - p, b - p] \subseteq [0, T]$, the following equality holds*

$$\int_a^b K(r)d\omega(r) = \int_{a-p}^{b-p} K(r + p)d\theta_p\omega(r).$$

4.3 Chemostat model driven by the fractional Brownian motion

As explained before, we are interested in investigating the stochastic chemostat model (4.1)-(4.2) perturbed by the fractional Brownian motion. To this end, we will firstly linearize our stochastic differential system around $(s_{in}, 0)$, the so-called *washout* equilibrium of the deterministic chemostat model given by (3)-(4), which allows us to rewrite the chemostat model (4.1)-(4.2) in the following abstract form

$$du = (Au + F(u))dt + G(u)dB^H(t), \tag{4.8}$$

where $u = (s, x)$, with

$$A = \begin{bmatrix} -D & -m + \frac{ma}{a+s_{in}} \\ 0 & -D + m - \frac{ma}{a+s_{in}} \end{bmatrix}, \qquad F(u) = \begin{bmatrix} Ds_{in} + \frac{ma}{a+S}x - \frac{ma}{a+s_{in}}x \\ -\frac{ma}{a+S}x + \frac{ma}{a+s_{in}}x \end{bmatrix}, \qquad G(u) = \begin{bmatrix} \alpha S \\ \alpha x \end{bmatrix}$$

and $B^H(\cdot)$ denotes the fBm.

Having reached this point, we state below three essential properties satisfied by the operators involved in (4.8).

(P1) G is differentiable and there exists $\delta \leq 1$ and $C_N > 0$, for every $N \geq 0$, such that the following properties are fulfilled:

- **Lispchitz Continuity**

$$|G(u) - G(\widehat{u})| \leq \alpha |u - \widehat{u}|, \quad \text{for all } u, \widehat{u} \in \mathbb{R}^d \text{ and every } t \in [0, T].$$

- **Local Hölder Continuity**

$$|\partial_{u_i} G(u) - \partial_{\widehat{u}_i} G(u)| \leq C_N |u - \widehat{u}|^{\delta}, \quad \text{for all } |u|, |\widetilde{u}| \leq N \text{ and every } t \in [0, T].$$

(P2) There exists $b_0 \in L^{\rho}([0, T]; \mathbb{R}^d)$, where $\rho \geq 2$, and $L_N > 0$, for every $N \geq 0$, such that the following properties hold:

- **Boundedness**

$$|Au + F(u)| \leq L_0 |u| + b_0, \quad \text{for all } u \in \mathbb{R}^d \text{ and every } t \in [0, T],$$

- **Local Lipschitz Continuity**

$$|(Au + F(u)) - (A\widehat{u} + F(\widehat{u})| \leq L_N |u - \widehat{u}|, \quad \text{for all } |u|, |\widehat{u}| \leq N \text{ and every } t \in [0, T],$$

(P3) It holds

$$|G(u)| \leq \alpha(1 + |u|), \quad \text{for all } u \in \mathbb{R}^d \text{ and every } t \in [0, T],$$

where $d = 2$ or $d = 3$ correspond to the stochastic chemostat model without taking into account the wall growth and with wall growth, respectively.

4.3.1 Existence and uniqueness of solution. Generation of an RDS

The following result establishes the existence and uniqueness of global solution of system (4.8).

Theorem 4.3.1 *Assume that $\beta \in (1/2, H)$. Then, for any $\omega \in \Omega$ and every initial pair $u_0 \in \mathbb{R}^2$, there exists a unique global solution of system* (4.8) *which belongs to $\mathscr{C}_{\beta}^{\beta}([0, T]; \mathbb{R}^2)$.*

We would like to remark that properties **(P1)-(P3)** are assumed in [68], where the authors consider a general stochastic differential equations driven by an fBm with $H > 1/2$ and analyze the existence and uniqueness of global solution of their system in some particular spaces. By following similar steps to those

carried out in [68], we can prove that there exists a unique solution $u \in \mathscr{C}_{\beta}^{\beta}([0,T];\mathbb{R}^2)$, hence the proof is omitted.

Remark 4.3.1 *We would like to note that the positiveness of the solutions of system* (4.1)-(4.2) *can be proved in this case by making use of the usual variable change*

$$\sigma(t) = s(t)e^{\alpha z_H^*(\theta_t\omega)} \qquad \text{and} \qquad \kappa(t) = x(t)e^{\alpha z_H^*(\theta_t\omega)},$$

where z_H^* denotes the stationary fractional Ornstein-Uhlenbeck process solving the Langevin equation

$$dz = -zdt + dB^H(t).$$

Since the ergodic properties are also true for z_H^* (see [22]), then we could transform the original stochastic system (4.1)-(4.2) *into another one with random coefficients, as made in Chapter 3. In such a way, it can be similarly prove that the resulting random system possesses a unique solution which remains in the positive cone for every initial value there.*

As pointed out, our aim in this chapter is not to perform the previous variable change but dealing directly with the stochastic system. Nevertheless, since we are dealing with a population model, even though it seems not to be possible to prove the positiveness of solutions without using this useful tool, decided to check that every solution is positive although the variable change is necessary for that.

We state now the following result concerning the generation of a C^0-semigroup by the matrix A.

Theorem 4.3.2 *Assume that*

$$D + \frac{ma}{a+s_{in}} > m \tag{4.9}$$

holds true. Then, system (4.8) *generates a C^0-semigroup operator, denoted by $S(\cdot)$, which is given by the fundamental solution $S(t) = e^{At}$, of the linear differential system $u' = Au$, where the matrix A is defined as in Section 4.3. In addition, the following estimates*

$$|S(t)| \leq Me^{-\lambda_1 t} \quad \text{and} \quad |S(t-s) - Id| \leq M|A|(t-s)e^{-\lambda_1(t-s)}$$

are fulfilled, with $M \geq 1$ and $\lambda_1 := D + \frac{ma}{a+s_{in}} - m$.

Proof. It trivially holds that matrix A generates a C^0-semigroup operator as long as condition (4.9) is fulfilled by analyzing the eigenvalues of the corresponding matrix A defining the abstract system (4.8). The rest of the statements follow directly from the definition of the semigroup.

□

Thanks to Theorem 4.3.2, the solution of (4.8) can be expressed by

$$u(t;\omega,u_0) = S(t)u_0 + \int_0^t S(t-s)F(u(s))ds + \int_0^t S(t-s)G(u(s))dB^H(s), \tag{4.10}$$

which is called *mild solution* and has the advantage that the semigroup operator will provide us some exponential terms with negative exponents which will be related to the dissipative ones needed to prove the existence and uniqueness of an absorbing set of our model, as we will see later.

Next, we prove that (4.8) generates a random dynamical system. Thanks to that, we will make use of the techniques already known concerning the theory of RDSs, as made in the previous chapters, and we will prove the existence and uniqueness of a random pullback attractor. To this end, we will define the following mapping

$$\varphi: \quad \mathbb{R}^+ \times \Omega \times \mathbb{R}^2_+ \quad \longrightarrow \quad \mathbb{R}^2_+,$$

where

$$\varphi(t,\omega)u_0 := S(t)u_0 + \int_0^t S(t-r)F(u(r))dr + \int_0^t S(t-r)G(u(r))d\omega(r). \tag{4.11}$$

Theorem 4.3.3 *System* (4.8) *generates a random dynamical system* $\{\varphi(t,\omega)\}_{t\geq 0,\omega\in\Omega}$ *defined by* (4.11).

Proof. On the one hand, for every initial pair $u_0 \in \mathbb{R}^2_+$, the mapping defined in (4.11) trivially satisfies that $\varphi(0,\omega)u_0 = S(0)u_0 = u_0$. On the other hand, from (4.11) and thanks to Lemma 4.2.2, for every initial value $u_0 \in \mathbb{R}^2_+$ and $t_1, t_2 \in \mathbb{R}^+$, it is easy to prove that the following equalities hold

$$\begin{aligned}
&\varphi(t_1+t_2,\omega)u_0\\
=\;& S(t_1+t_2)u_0 + \int_0^{t_1+t_2} S(t_1+t_2-r)F(u(r))dr + \int_0^{t_1+t_2} S(t_1+t_2-r)G(u(r))d\omega(r)\\
=\;& S(t_1)S(t_2)u_0 + \int_0^{t_2} S(t_1)S(t_2-r)F(u(r))dr + \int_0^{t_2} S(t_1)S(t_2-r)G(u(r))d\omega(r)\\
&+ \int_{t_2}^{t_1+t_2} S(t_1+t_2-r)F(u(r))dr + \int_{t_2}^{t_1+t_2} S(t_1+t_2-r)G(u(r))d\omega(r)\\
=\;& S(t_1)\varphi(t_2,\omega)u_0 + \int_0^{t_1} S(t_1-r)F(u(r+t_2))dr + \int_0^{t_1} S(t_1-r)G(u(r+t_2))d\theta_{t_2}\omega(r)\\
=\;& \varphi(t_1,\theta_{t_2}\omega)\varphi(t_2,\omega)u_0,
\end{aligned}$$

whence we obtain the cocycle property. In addition, since φ is $(\mathscr{B}(\mathbb{R}^+)\times\mathscr{F}\times\mathscr{B}(\mathbb{R}^2_+),\mathscr{B}(\mathbb{R}^2_+))$–measurable, the result is proved.

□

4.3.2 Asymptotic dynamics of the chemostat model with fBm

In this section we start proving the existence of a discrete tempered compact random absorbing set. To this end, we firstly need to estimate the norm of the solution of system (4.8) for which the following lemma is helpful.

Lemma 4.3.1 *For every $T > 0$, $\omega \in \Omega$ and $\beta > 1/2$, we have*

$$\begin{aligned}\left\| \int_0^{\cdot} S(\cdot - r) F(u(r)) dr \right\|_{\beta,\beta,0,T} &\leq c_{S,F} T \left(1 + \|u\|_{\beta,\beta,0,T}\right), \\ \left\| \int_0^{\cdot} S(\cdot - r) G(u(r)) d\omega \right\|_{\beta,\beta,0,T} &\leq c_{S,G} T^{\beta} \|u\|_{\beta,\beta,0,T} |||\omega|||_{\beta,0,T},\end{aligned}$$

where $c_{S,F}$ and $c_{S,G}$ refers to constants related to the semigroup operator as well as the operators F and G, respectively.

Proof. The proof of the norm of the deterministic integral follows trivially since the corresponding integral is defined in the sense of Lebesgue whereas the norm of the stochastic integral can be obtained by taking into account the estimate (4.7) in Lemma 4.2.2 and the estimates of the semigroup stated in Theorem 4.3.2.

□

Thanks to Lemma 4.3.1 we can deduce the following estimate for the norm of the solution of system (4.8).

Theorem 4.3.4 *For any $\omega \in \Omega$ and every $T > 0$, we have the following estimate*

$$\|u\|_{\beta,\beta,0,T} \leq c_S |u_0| + c_{S,F} T \left(1 + \|u\|_{\beta,\beta,0,T}\right) + c_{S,G} T^{\beta} |||\omega|||_{\beta,0,T} \|u\|_{\beta,\beta,0,T}, \tag{4.12}$$

where c_S denotes a constant coming from the semigroup operator and the constants $c_{S,F}$ and $c_{S,G}$ has been introduced in Lemma 4.3.1.

Proof. The first addend on the right side of (4.12) follows trivially by taking into account the properties satisfied by the semigroup operator, stated in Theorem 4.3.2. Concerning the rest of the terms in (4.12), they directly follows from the estimates in Lemma 4.3.1.

□

From (4.12), it is easy to notice that it is not possible to conclude anything for $\|u\|_{\beta,\beta,0,T}$ since the size of $|||\omega|||_{\beta,0,T}$ could be arbitrary large. As a consequence, it is not possible to make use of any Gronwall's Lemma in order to obtain some bound of the norm of the solution of system (4.8). Because of this reason, we will introduce a sequence of stopping times, which will be denoted by $\{T_i(\omega)\}_{i\in\mathbb{Z}}$, which will allow us to control the size of every element of the sequence $\{|||\omega|||_{\beta,T_i(\omega),T_{i+1}(\omega)}\}_{i\in\mathbb{Z}}$ for any realization of the noise and, therefore, to prove the existence of a discrete tempered compact random absorbing set. To this end, let us consider now a real constant $\mu \in (0,1)$. Then, we define $T(\omega) \equiv T_1(\omega)$ and $\widehat{T}(\omega) \equiv T_{-1}(\omega)$ as follows

$$\begin{aligned}|||\omega|||_{\beta,0,T(\omega)}\, T(\omega)^{\beta} + T(\omega) &= \mu, \\ |||\omega|||_{\beta,\widehat{T}(\omega),0}(-\widehat{T}(\omega))^{\beta} + (-\widehat{T}(\omega)) &= \mu.\end{aligned} \tag{4.13}$$

From (4.13), we can consider the following sequence of stopping times $\{T_i(\omega)\}_{i\in\mathbb{Z}}$, which can be defined, for every $i, j \in \mathbb{Z}$ and any $\omega \in \Omega$, as follows

$$T_0(\omega) = 0, \qquad T_i(\omega) + T_j(\theta_{T_i(\omega)}\omega) = T_{i+j}(\omega). \tag{4.14}$$

For a detailed description of the stopping times, see Section 4.3.3.

Now we can state the following essential result concerning an estimate of the norm of the solution of system (4.8) in some interval given by two consecutive stopping times previously defined.

Theorem 4.3.5 *For every $\omega \in \Omega$ and $\beta > 1/2$ we consider $\{T_i(\theta_{T_j}\omega)\}_{i\in\mathbb{Z}}$, the sequence of stopping times defined in* (4.14) *for the noise path $\theta_{T_j}\omega$, with $j \in \mathbb{Z}$. Then, the following estimate holds for the solution of* (4.10)

$$\begin{aligned}\|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} \leq\ & ce^{-\lambda_1 T_n(\theta_{T_j}\omega)}|u_0| + c\mu\sum_{m=1}^{n} e^{-\lambda_1(T_n(\theta_{T_j}\omega)-T_m(\theta_{T_j}\omega))} \\ & + c\mu\sum_{m=1}^{n} e^{-\lambda_1(T_n(\theta_{T_j}\omega)-T_m(\theta_{T_j}\omega))}\|u\|_{\beta,\beta,T_{m-1}(\theta_{T_j}\omega),T_m(\theta_{T_j}\omega)} \\ & + c\mu\|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} + c\mu,\end{aligned} \tag{4.15}$$

where c denotes a positive constant depending on c_S, $c_{S,F}$ and $c_{S,G}$.

Proof. In order to prove (4.15) we just provide the most important calculations since a similar one can be found in [30, 37]. To this end, for $t \in [T_n(\theta_{T_j}\omega), T_{n+1}(\theta_{T_j}\omega)]$ we have the following splitting

$$\begin{aligned} u(t) =\ & S(t)u_0 + \sum_{m=1}^{n}\int_{T_{m-1}(\theta_{T_j}\omega)}^{T_m(\theta_{T_j}\omega)} S(t-r)F(u(r))dr + \sum_{m=1}^{n}\int_{T_{m-1}(\theta_{T_j}\omega)}^{T_m(\theta_{T_j}\omega)} S(t-r)G(u(r))d\theta_{T_j}\omega \\ & + \int_{T_n(\theta_{T_j}\omega)}^{t} S(t-r)F(u(r))dr + \int_{T_n(\theta_{T_j}\omega)}^{t} S(t-r)G(u(r))d\theta_{T_j}\omega \\ =\ & S(t)u_0 + \sum_{m=1}^{n}\int_{0}^{T_m(\theta_{T_j}\omega)-T_{m-1}(\theta_{T_j}\omega)} S(t-T_{m-1}(\theta_{T_j}\omega)-r)F(u(r+T_{m-1}(\theta_{T_j}\omega)))dr \\ & + \sum_{m=1}^{n}\int_{0}^{T_m(\theta_{T_j}\omega)-T_{m-1}(\theta_{T_j}\omega)} S(t-T_{m-1}(\theta_{T_j}\omega)-r)G(u(r+T_{m-1}(\theta_{T_j}\omega)))d\theta_{T_{j+m-1}}\omega \\ & + \int_{0}^{t-T_n(\theta_{T_j}\omega)} S(t-T_n(\theta_{T_j}\omega)-r)F(u(r+T_n(\theta_{T_j}\omega)))dr \\ & + \int_{0}^{t-T_n(\theta_{T_j}\omega)} S(t-T_n(\theta_{T_j}\omega)-r)G(u+T_n(\theta_{T_j}\omega))d\theta_{T_{j+n}}\omega \end{aligned}$$

Environmental effects caused by the fractional Brownian motion

$$
\begin{aligned}
= \quad & S(t)u_0 + \sum_{m=1}^{n} S(t - T_m(\theta_{T_j}\omega)) \int_0^{T_1(\theta_{T_{j+m-1}}\omega)} S(T_1(\theta_{T_{j+m-1}}\omega) - r) F(u(r + T_{m-1}(\theta_{T_j}\omega)))\, dr \\
& + \sum_{m=1}^{n} S(t - T_m(\theta_{T_j}\omega)) \int_0^{T_1(\theta_{T_{j+m-1}}\omega)} S(T_1(\theta_{T_{j+m-1}}\omega) - r) G(u(r + T_{m-1}(\theta_{T_j}\omega)))\, d\theta_{T_{j+m-1}}\omega \\
& + \int_0^{t - T_n(\theta_{T_j}\omega)} S(t - T_n(\theta_{T_j}\omega) - r) F(u(r + T_n(\theta_{T_j}\omega)))\, dr \\
& + \int_0^{t - T_n(\theta_{T_j}\omega)} S(t - T_n(\theta_{T_j}\omega) - r) G(u(r + T_n(\theta_{T_j}\omega)))\, d\theta_{T_{j+n}}\omega, \qquad (4.16)
\end{aligned}
$$

where we wrote $u(t)$ instead of $u(t;\omega,u_0)$ for the sake of space.

Then, on account of Lemma 4.3.1, we can estimate the norm of each term in (4.16) obtaining that

$$
\begin{aligned}
& \|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} \le c e^{-\lambda_1 T_n(\theta_{T_j}\omega)} |u_0| \\
& + c \sum_{m=1}^{n} e^{-\lambda_1 (T_n(\theta_{T_j}\omega) - T_m(\theta_{T_j}\omega))} T_1(\theta_{T_{j+m-1}}\omega) \left(1 + \|u\|_{\beta,\beta,T_{m-1}(\theta_{T_j}\omega),T_m(\theta_{T_j}\omega)}\right) \\
& + c \sum_{m=1}^{n} e^{-\lambda_1 (T_n(\theta_{T_j}\omega) - T_m(\theta_{T_j}\omega))} T_1(\theta_{T_{j+m-1}}\omega)^{\beta} \|u\|_{\beta,\beta,T_{m-1}(\theta_{T_j}\omega),T_m(\theta_{T_j}\omega)} |||\theta_{T_{j+m-1}}\omega|||_{\beta,0,T_1(\theta_{T_{j+m-1}}\omega)} \\
& + c T_1(\theta_{T_{j+n}}\omega) \left(1 + \|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)}\right) \\
& + c T_1(\theta_{T_{j+n}}\omega)^{\beta} \|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} |||(\theta_{T_{j+n}}\omega)|||_{\beta,0,T_1(\theta_{T_{j+n}}\omega)},
\end{aligned}
$$

where c is a constant depending on the semigroup and both operators F and G.

Hence, by taking into account the definition of the first stopping time given by (4.13), the inequality (4.15) easily follows.

□

As a result, defining

$$
k_0 = \frac{c}{1 - c\mu} \qquad \text{and} \qquad k_1 = \frac{c\mu}{1 - c\mu},
$$

from (4.15) we obtain

$$
\|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} \le k_0 e^{-\lambda_1 T_n(\theta_{T_j}\omega)} |u_0| + k_1 \sum_{m=1}^{n} e^{-\lambda_1 (T_n(\theta_{T_j}\omega) - T_m(\theta_{T_j}\omega))} \|u\|_{\beta,\beta,T_{m-1}(\theta_{T_j}\omega),T_m(\theta_{T_j}\omega)}
$$

$$+k_1 \sum_{m=1}^{n} e^{-\lambda_1 (T_n(\theta_{T_j}\omega) - T_m(\theta_{T_j}\omega))} + k_1. \tag{4.17}$$

The following natural step consists in introducing a discrete random dynamical system which is defined as the restriction of the original continuous random dynamical system to the sequence of stopping times $\{T_i(\omega)\}_{i\in\mathbb{Z}}$ given by (4.14). More precisely, we firstly introduce the new discrete shift, which is given by the mapping

$$\begin{aligned} \widetilde{\theta}: \quad \mathbb{Z}\times\mathbb{Z} &\longrightarrow \mathbb{Z} \\ (i,j) &\longmapsto \widetilde{\theta}(i,j) \equiv \widetilde{\theta}_i\, j := i + j \end{aligned}$$

that satisfies the following properties: on the one hand, the mapping $\widetilde{\theta}_0$ is trivially the identity operator in $\mathbb{Z}$; on another hand, the cocycle property

$$\widetilde{\theta}_{i_1+i_2}\, j = (\widetilde{\theta}_{i_1} \circ \widetilde{\theta}_{i_2})\, j$$

also holds. Now, we introduce the following mapping

$$\Phi: \quad \mathbb{Z}^+ \times \mathbb{Z} \times \Omega \times \mathbb{R}^2_+ \longrightarrow \mathbb{R}^2_+,$$

defined by

$$\Phi(i,j,\omega,u_0) := \varphi(T_i(\theta_{T_j(\omega)}\omega), \theta_{T_j(\omega)}\omega, u_0), \tag{4.18}$$

the solution given by (4.10) at time $T_i(\theta_{T_j(\omega)}\omega)$ for the noise path $\theta_{T_j(\omega)}\omega$.

We would like to emphasize that ω only acts as a parameter in (4.18). Apart from that, for the sake of simplicity, we write $\theta_{T_j}\omega$ instead of $\theta_{T_j(\omega)}\omega$ when no confusion is possible.

It is not difficult to prove that the mapping given by (4.18) is actually a discrete dynamical system. The proof of this statement follows trivially from its definition since the property is inherited from the original continuous random dynamical system $\{\varphi(t,\omega)\}_{t\geq 0,\omega\in\Omega}$.

Now, we make use of the estimate (4.17) to prove the existence of a discrete absorbing set which allows us to conclude that there exists a unique discrete random pullback attractor associate to the discrete dynamical system defined by (4.18).

Henceforth, we will denote the discrete tempered sets by $E(i,\omega)$, where $i \in \mathbb{Z}$ and $\omega \in \Omega$ acts as a parameter. In addition, $\rho(i,\omega)$ will denote the radius of the corresponding discrete tempered set previously mentioned.

Theorem 4.3.6 *Assume that for $\omega \in \Omega$, there exists $D > 0$ such that*

$$\lambda_1 D > k_1 e^{\lambda_1 \mu} \tag{4.19}$$

and

$$\liminf_{q\to-\infty}\frac{|T_q(\theta_{T_j}\omega)|}{|q|}>D \tag{4.20}$$

hold true for the noise path $\theta_{T_j}(\omega)$, where $j\in\mathbb{Z}$. Then, there exists a tempered discrete absorbing set associated to the discrete dynamical system (4.18)*, which is given by the ball centered at the origin with radius*

$$R(j,\omega):=2k_1\sum_{q=-\infty}^{0}e^{\lambda_1 T_q(\theta_{T_j}\omega)}e^{-k_1 q e^{\lambda_1\mu}}, \tag{4.21}$$

where $T_q(\cdot)$ denotes the $q-$stopping time for $q\in\mathbb{Z}$.

Proof. After multiplying (4.17) by the factor $e^{\lambda_1 T_n(\theta_{T_j}\omega)}$, we have

$$\begin{aligned}
& e^{\lambda_1 T_n(\theta_{T_j}\omega)}\|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)}\\
\leq\ & k_0|u_0|+k_1\sum_{m=1}^{n}e^{\lambda_1 T_m(\theta_{T_j}\omega)}e^{-\lambda_1 T_{m-1}(\theta_{T_j}\omega)}e^{\lambda_1 T_{m-1}(\theta_{T_j}\omega)}\|u\|_{\beta,\beta,T_{m-1}(\theta_{T_j}\omega),T_m(\theta_{T_j}\omega)}\\
& +k_1\sum_{m=1}^{n}e^{\lambda_1 T_m(\theta_{T_j}\omega)}+k_1e^{\lambda_1 T_n(\theta_{T_j}\omega)},\\
=\ & k_0|u_0|+k_1\sum_{m=0}^{n-1}e^{\lambda_1 T_1(\theta_{T_{m+j}}\omega)}e^{\lambda_1 T_m(\theta_{T_j}\omega)}\|u\|_{\beta,\beta,T_m(\theta_{T_j}\omega),T_{m+1}(\theta_{T_j}\omega)}\\
& +k_1\sum_{m=0}^{n-1}e^{\lambda_1 T_{m+1}(\theta_{T_j}\omega)}+k_1e^{\lambda_1 T_n(\theta_{T_j}\omega)},
\end{aligned}$$

whence, considering y_k defined as $y_k:=e^{\lambda_1 T_k(\theta_{T_j}\omega)}\|u\|_{\beta,\beta,T_k(\theta_{T_j}\omega),T_{k+1}(\theta_{T_j}\omega)}$, we have

$$y_n\ \leq\ k_0|u_0|+k_1\sum_{m=0}^{n-1}e^{\lambda_1 T_1(\theta_{T_{m+j}}\omega)}y_m+2k_1\sum_{m=0}^{n-1}e^{\lambda_1 T_{m+1}(\theta_{T_j}\omega)}.$$

Now, we define the positive functions

$$f_n:=k_0|u_0|+2k_1\sum_{m=1}^{n}e^{\lambda_1 T_m(\theta_{T_j}\omega)}\quad\text{and}\quad g_k:=k_1e^{\lambda_1 T_1(\theta_{T_{k+j}}\omega)}, \tag{4.22}$$

and consider

$$\psi_0:=k_0|u_0|\qquad\text{and}\qquad\psi_q:=2k_1e^{\lambda_1 T_q(\theta_{T_j}\omega)}. \tag{4.23}$$

Hence, thanks to (4.22) and (4.23), applying the discrete Gronwall lemma C.0.4 (see Appendix C), we

obtain that

$$\begin{aligned} y_n &\leq k_0|u_0|\prod_{l=0}^{n-1}\left(1+k_1 e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}\right)+2k_1\sum_{q=1}^{n} e^{\lambda_1 T_q(\theta_{T_j}\omega)}\prod_{l=q}^{n-1}\left(1+k_1 e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}\right) \\ &\leq k_0|u_0|\prod_{l=0}^{n-1} e^{k_1 e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}}+2k_1\sum_{q=1}^{n} e^{\lambda_1 T_q(\theta_{T_j}\omega)}\prod_{l=q}^{n-1} e^{k_1 e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}} \\ &= k_0|u_0|e^{k_1\sum_{l=0}^{n-1} e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}}+2k_1\sum_{q=1}^{n} e^{\lambda_1 T_q(\theta_{T_j}\omega)} e^{k_1\sum_{l=q}^{n-1} e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}} \\ &\leq k_0|u_0|e^{k_1 n e^{\lambda_1\mu}}+2k_1\sum_{q=1}^{n} e^{\lambda_1 T_q(\theta_{T_j}\omega)} e^{k_1(n-q)e^{\lambda_1\mu}}, \end{aligned}$$

where the last inequality holds since $T_1(\theta_{T_{l+j}}\omega)\leq\mu$, then

$$\sum_{l=0}^{n-1} e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}\leq\sum_{l=0}^{n-1} e^{\lambda_1\mu}=ne^{\lambda_1\mu}\quad\text{and}\quad\sum_{l=q}^{n-1} e^{\lambda_1 T_1(\theta_{T_{l+j}}\omega)}\leq(n-q)e^{\lambda_1\mu}.$$

Hence, we obtain the final bound for the norm of our solution, which is given by

$$\begin{aligned} \|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} &\leq k_0|u_0|e^{k_1 n e^{\lambda_1\mu}} e^{-\lambda_1 T_n(\theta_{T_j}\omega)} \\ &\quad +2k_1\sum_{q=1}^{n} e^{\lambda_1 T_q(\theta_{T_j}\omega)} e^{-\lambda_1 T_n(\theta_{T_j}\omega)} e^{k_1(n-q)e^{\lambda_1\mu}}. \end{aligned}$$

Now, thanks to the definition of the discrete dynamical system (4.18), we have that

$$\begin{aligned} |\Phi(n,j,\omega,u_0)| &\leq \|u\|_{\beta,\beta,T_n(\theta_{T_j}\omega),T_{n+1}(\theta_{T_j}\omega)} \\ &\leq k_0|u_0|e^{k_1 n e^{\lambda_1\mu}} e^{-\lambda_1 T_n(\theta_{T_j}\omega)}+2k_1\sum_{q=1}^{n} e^{\lambda_1 T_q(\theta_{T_j}\omega)} e^{-\lambda_1 T_n(\theta_{T_j}\omega)} e^{k_1(n-q)e^{\lambda_1\mu}}. \end{aligned} \tag{4.24}$$

By replacing j by $\widetilde{\theta}_{-n}j=j-n$ in (4.24) and taking supremum, we obtain

$$\begin{aligned} &\sup_{u_0\in E(j-n,\omega)}|\Phi(n,j-n,\omega,u_0)| \\ &\leq k_0\rho(j-n,\omega)e^{k_1 n e^{\lambda_1\mu}} e^{-\lambda_1 T_n(\theta_{T_{j-n}}\omega)}+2k_1\sum_{q=1-n}^{0} e^{\lambda_1 T_{q+n}(\theta_{T_{j-n}}\omega)-\lambda_1 T_n(\theta_{T_{j-n}}\omega)} e^{-k_1 q e^{\lambda_1\mu}} \\ &= k_0\rho(j-n,\omega)e^{k_1 n e^{\lambda_1\mu}} e^{-\lambda_1 T_n(\theta_{T_{j-n}}\omega)}+2k_1\sum_{q=1-n}^{0} e^{\lambda_1 T_q(\theta_{T_j}\omega)} e^{-k_1 q e^{\lambda_1\mu}}, \end{aligned} \tag{4.25}$$

where $\rho(j-n,\omega)$ denotes the radius of the discrete tempered set $E(j-n,\omega)$.

Now, by taking limit when n tends to infinity in (4.25), we have

$$\begin{aligned}&\lim_{n\to+\infty}\sup_{u_0\in E(j-n,\omega)}|\Phi(n,j-n,\omega,u_0)|\\ \leq\ &\lim_{n\to+\infty}k_0\rho(j-n,\omega)e^{k_1ne^{\lambda_1\mu}}e^{-\lambda_1T_n(\theta_{T_{j-n}}\omega)}+2k_1\sum_{q=-\infty}^{0}e^{\lambda_1T_q(\theta_{T_j}\omega)}e^{-k_1qe^{\lambda_1\mu}}.\end{aligned}\tag{4.26}$$

Before analyzing the addends in (4.26) in more detail, we would like to notice that, thanks to (4.20), for every $\varepsilon>0$ there exists $q_\varepsilon>0$ such that for $|q|>q_\varepsilon$, we have that $T_q(\theta_{T_j}\omega)<q(D-\varepsilon)$. Hence, since λ_1 is a positive constant, we have

$$\lambda_1T_q(\theta_{T_j}\omega)-k_1qe^{\lambda_1\mu}\ <\ q\left[\lambda_1D-k_1e^{\lambda_1\mu}-\lambda_1\varepsilon\right].$$

Now, we analyze the addends in (4.26). On the one hand, by taking into account (4.20), for $\widehat{M}>0$ large enough we obtain that

$$\begin{aligned}R(j,\omega)\ &:=\ 2k_1\sum_{q=-\infty}^{0}e^{\lambda_1T_q(\theta_{T_j}\omega)}e^{-k_1qe^{\lambda_1\mu}}\\ &<\ 2k_1\left(\sum_{q=-\widehat{M}}^{0}e^{\lambda_1T_q(\theta_{T_j}\omega)-k_1qe^{\lambda_1\mu}}+\sum_{q=-\infty}^{-\widehat{M}-1}e^{q[\lambda_1D-k_1e^{\lambda_1\mu}-\lambda_1\varepsilon]}\right),\end{aligned}\tag{4.27}$$

where the last term in (4.27) is well defined thanks to (4.19).

On the other hand, we analyze the term given by the limit in (4.26). To this end, for $\varepsilon>0$ small enough, $\zeta:=D\lambda_1-k_1e^{\lambda_1\mu}-\varepsilon\lambda_1>0$. Then, thanks to (4.19), (4.20) and the fact that $-T_n(\theta_{T_{j-n}}\omega)=T_{-n}(\theta_{T_j}\omega)$, we have that

$$\begin{aligned}\lim_{n\to+\infty}k_0\rho(j-n,\omega)e^{k_1ne^{\lambda_1\mu}}e^{-\lambda_1T_n(\theta_{T_{j-n}}\omega)}\ &=\ \lim_{n\to+\infty}k_0\rho(j-n,\omega)e^{k_1ne^{\lambda_1\mu}}e^{\lambda_1T_{-n}(\theta_{T_j}\omega)}\\ &\leq\ \lim_{n\to+\infty}k_0\rho(j-n,\omega)e^{k_1ne^{\lambda_1\mu}}e^{-Dn\lambda_1+\varepsilon n\lambda_1}\\ &=\ k_0e^{-\zeta j}\lim_{n\to+\infty}\rho(j-n,\omega)e^{\zeta(j-n)}=0.\end{aligned}$$

Summing up, from the previous calculations, we deduce that

$$\lim_{n\to+\infty}\sup_{u_0\in E(j-n,\omega)}|\Phi(n,j-n,\omega,u_0)|\leq 2k_1\sum_{q=-\infty}^{0}e^{\lambda_1T_q(\theta_{T_j}\omega)}e^{-k_1qe^{\lambda_1\mu}}=R(j,\omega).$$

Having reached this point, it remains to check that the radius $R(j,\omega)$ given by (4.21) is tempered, which

means that

$$\lim_{j\to-\infty} e^{\delta j} R(j,\omega) = 0.$$

We omit the proof of the temperedness of $R(j,\omega)$ since it can be easily made by using similar arguments to the ones shown before.

In conclusion, we deduce that the ball centered at the origin with radius given by (4.21) is a tempered discrete absorbing set which will be denoted by $\left\{B(j,\omega)\right\}_{j\in\mathbb{Z},\omega\in\Omega}$.

□

From Theorem 4.3.6, thanks to Proposition B.0.1 in Appendix B, we deduce that there exists a unique discrete random pullback attractor, which will be denoted by $\{\mathscr{A}(i,\omega)\}_{i\in\mathbb{Z},\omega\in\Omega}$, associated to the discrete dynamical system $\{\Phi(i,j)\}_{i,j\in\mathbb{Z}}$ given by (4.18), as presented in the following result.

Proposition 4.3.1 *The discrete dynamical system* (4.18) *has a discrete random pullback attractor* $\{\mathscr{A}(i,\omega)\}_{i\in\mathbb{Z},\omega\in\Omega}$ *given by*

$$\mathscr{A}(i,\omega) = \bigcap_{n\in\mathbb{N}} \overline{\bigcup_{m\geq n} \Phi\left(m,-m+i,\omega,B(-m+i,\omega)\right)}, \tag{4.28}$$

where B *denotes the absorbing ball obtained in Theorem 4.3.6.*

We also remark that the measurability of the discrete random pullback attractor given by (4.28) follows trivially since the stopping times are measurable.

To finish the section, we prove a result concerning the existence and uniqueness of continuous random pullback attractor, which will coincide with the component $\{\mathscr{A}(0,\omega)\}_{\omega\in\Omega}$ of the discrete one, associated to the continuous RDS (4.11).

Theorem 4.3.7 *There exists a unique continuous random pullback attractor associated to the continuous random dynamical system* $\{\varphi(t,\omega)\}_{t\geq 0,\omega\in\Omega}$*, which is given by* $\{\mathscr{A}(\omega)\}_{\omega\in\Omega}$*, where* $\mathscr{A}(\omega)$ *is defined as the component* $\{\mathscr{A}(0,\omega)\}_{\omega\in\Omega}$ *of the discrete random attractor associated to the discrete random dynamical system* (4.18).

Proof. The proof of this result is omitted since it is exactly the same that the one in [37]. We would like just to note that one of the main ingredients is the relation between the continuous and discrete tempered sets. In fact, if J be a continuous tempered set, then

$$E_J(i,\omega) = \overline{\bigcup_{-\tau\in[\hat{T}(\theta_{T_i}\omega),0]} \bigcup_{u_0\in E(\theta_{-\tau}\theta_{T_i}\omega)} \{\varphi(\tau,\theta_{-\tau}\theta_{T_i}\omega,u_0)\}}$$

defines discrete tempered set. Moreover,

$$E_H(i,\omega) = \overline{\bigcup_{\tau\in[0,T(\theta_{T_i}\omega)]} \bigcup_{u_0\in E(i,\omega)} \{\varphi(\tau,\theta_{T_i}\omega,u_0)\}}$$

is a discrete tempered set as long as H is a discrete tempered set as well. Once taken that into account, the proof basically consists on checking that $\{\mathscr{A}(0,\omega)\}_{\omega\in\Omega}$ is compact, invariant and attracting or, in other

words, every property in Definition B.0.5 in Appendix B holds.

□

4.3.3 Analysis of stopping times

In this section, we develop a deeper analysis of the sequence of stopping times given by (4.14). We will firstly state an estimation of the random number of stopping times on the interval $(0, \mu]$, which allows us to prove a result concerning the distribution of those stopping times on the whole real line. Thanks to this, we will deduce that the sequence of stopping times $\{T_i(\omega)\}_{i\in\mathbb{Z}}$ has no accumulation points and, therefore, it completely covers the real line. In addition, this last result will guarantee that condition (4.19) in Lemma 4.3.6 can be assumed by taking small enough noise.

Firstly, for $H > 1/2$, we set $1/2 < \beta < \beta' < H$. Thus, let us consider Ω the $\{\theta_t\}_{t\in\mathbb{R}}-$invariant set of paths $\omega : \mathbb{R} \to \mathbb{R}$ which are $\beta'-$Hölder continuous on any compact subinterval of the real line and are zero at zero. Then, Ω is $\{\theta_t\}_{t\in\mathbb{R}}-$invariant (see [21]).

Lemma 4.3.2 *Let $\omega \in \Omega$. The mapping $t \mapsto |||\omega|||_{\beta',0,t}$ is continuous on $\mathbb{R}^+$, and the mapping $t \mapsto |||\omega|||_{\beta',t,0}$ is continuous on $\mathbb{R}^-$.*

Proof. We only prove the continuity of the first mapping since the second one can be treated similarly. To this end, if $t \geq t_0$, let us define ω^{t_0} as follows

$$\omega^{t_0}(s) = \begin{cases} \omega(s), & \text{for} \quad s < t_0, \\ \omega(t_0), & \text{for} \quad s \geq t_0. \end{cases}$$

Thus, for $t \geq t_0$ we have

$$\left|\,|||\omega|||_{\beta,0,t} - |||\omega|||_{\beta,0,t_0}\,\right| = \left|\,|||\omega|||_{\beta,0,t} - |||\omega^{t_0}|||_{\beta,0,t}\,\right| \leq |||\omega - \omega^{t_0}|||_{\beta,0,t} = |||\omega|||_{\beta,t_0,t},$$

whence

$$\begin{aligned} \limsup_{t\to t_0}\left|\,|||\omega|||_{\beta,0,t} - |||\omega|||_{\beta,0,t_0}\,\right| &\leq \limsup_{t\to t_0}\left(|||\omega|||_{\beta',t_0,t}(t-t_0)^{\beta'-\beta}\right) \\ &\leq \limsup_{t\to t_0}|||\omega|||_{\beta',0,t}\lim_{t\to t_0}(t-t_0)^{\beta'-\beta} = 0, \end{aligned}$$

then, by the same argument, we can deduce that

$$\liminf_{t\to t_0}\left|\,|||\omega|||_{\beta,0,t} - |||\omega|||_{\beta,0,t_0}\,\right| = 0.$$

Hence,

$$\lim_{t\to t_0}|||\omega|||_{\beta,0,t} = |||\omega|||_{\beta,0,t_0}.$$

We note that the case $t \leq t_0$ can be proved similarly.

□

We would like to remark that the stopping time $T(\omega)$ given by (4.13) is well defined and, in addition, it satisfies $T(\omega) \in (0, \mu]$.

As we explained in the last paragraph, we begin providing an estimate of the number of stopping times on the interval $(0, \mu]$ which is stated in the next result.

Proposition 4.3.2 *Let $N(\omega) \in \mathbb{N}$ be the random number of stopping times in $(0, \mu]$. Then, for $\omega \in \Omega$, we have*

$$N(\omega) \leq \mu \left(\frac{|||\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu} \right)^{\frac{1}{\beta'}}. \tag{4.29}$$

In addition,

$$\limsup_{n\to+\infty} \frac{1}{\mu n} \sum_{i=0}^{n-1} N(\theta_{i\mu}\omega) \leq \mathbb{E}\left(\sup_{r\in[-\mu,0]} \left(\frac{|||\theta_r\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu} \right)^{\frac{1}{\beta'}} \right) =: \frac{1}{\mu d} \tag{4.30}$$

for all ω in a $\{\theta_t\}_{t\in\mathbb{R}}-$invariant set of full measure where $d = d(\mu, \omega) \in (0, 1]$.

Proof. For every $\omega \in \Omega$, since $T(\omega) < \mu$, thanks to (4.13) we have

$$\begin{aligned}
\mu &= \sup_{0\leq s<t\leq T(\omega)} \frac{|\omega(t)-\omega(s)|}{|t-s|^{\beta'}} |t-s|^{\beta'-\beta} T(\omega)^{\beta} + T(\omega) \\
&\leq |||\omega|||_{\beta',0,T(\omega)} T(\omega)^{\beta'-\beta} T(\omega)^{\beta} + T(\omega) \\
&= T(\omega)^{\beta'} \left[|||\omega|||_{\beta',0,T(\omega)} + T(\omega)^{1-\beta'} \right] \\
&< T(\omega)^{\beta'} \left[|||\omega|||_{\beta',0,\mu} + \mu^{1-\beta'} \right]
\end{aligned}$$

whence we obtain

$$T(\omega) \geq \left(\frac{\mu}{|||\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}} \right)^{\frac{1}{\beta'}}.$$

The same bound can be proved for $T(\theta_{T_i(\omega)}\omega)$ as long as $T_{i+1}(\omega) \leq \mu$, as follows

$$\begin{aligned}
\mu &= |||\theta_{T_i(\omega)}\omega|||_{\beta,0,T(\theta_{T_i(\omega)}\omega)} T(\theta_{T_i(\omega)}\omega)^{\beta} + T(\theta_{T_i(\omega)}\omega) \\
&\leq |||\omega|||_{\beta',T_i(\omega),T_{i+1}(\omega)} T(\theta_{T_i(\omega)}\omega)^{\beta'-\beta} T(\theta_{T_i(\omega)}\omega)^{\beta} + T(\theta_{T_i(\omega)}\omega)
\end{aligned}$$

$$\leq \quad T(\theta_{T_i(\omega)}\omega)^{\beta'}\left[|||\omega|||_{\beta',0,\mu} + T(\theta_{T_i(\omega)}\omega)^{1-\beta'}\right],$$

thus, we have

$$T(\theta_{T_i(\omega)}\omega) \geq \left(\frac{\mu}{|||\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}\right)^{\frac{1}{\beta'}}.$$

By definition, $N(\omega)$ is the largest number such that $T_{N(\omega)}(\omega) \leq \mu$. Then, thanks to the definition of the stopping times (4.14) we obtain

$$\mu \geq T_{N(\omega)}(\omega) = \sum_{i=0}^{N(\omega)-1} T(\theta_{T_i(\omega)}(\omega)) \geq N(\omega)\left(\frac{\mu}{|||\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}\right)^{\frac{1}{\beta'}},$$

whence we can easily deduce (4.29).

Now, let us note that $\sup_{r\in[-\mu,0]} |||\theta_r\omega|||_{\beta',0,\mu} \leq |||\omega|||_{\beta',-\mu,\mu}$ and the right side of the last equality has finite moments, then (see [58]) we have

$$\mathbb{E}\left(\sup_{r\in[-\mu,0]}\left(\frac{|||\theta_r\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}}\right) < +\infty.$$

In fact, since

$$N(\theta_{i\mu}\omega) \leq \mu\left(\frac{|||\theta_{i\mu}\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}} \leq \int_0^{\mu} \sup_{r\in[-\mu,0]}\left(\frac{|||\theta_{r+q+i\mu}\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}} dq$$

and thanks to Lemma 4.2.2, we have

$$\begin{aligned}\sum_{i=0}^{n-1} N(\theta_{i\mu}\omega) \quad &\leq \quad \sum_{i=0}^{n-1}\int_0^{\mu} \sup_{r\in[-\mu,0]}\left(\frac{|||\theta_{r+q+i\mu}\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}} dq \\ &= \quad \int_0^{\mu n} \sup_{r\in[-\mu,0]}\left(\frac{|||\theta_{r+q}\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}} dq,\end{aligned}$$

whence we can deduce (4.30) since

$$\begin{aligned}\limsup_{n\to+\infty} \frac{1}{\mu n}\sum_{j=0}^{n-1} N(\theta_{i\mu}\omega) \quad &\leq \quad \lim_{n\to+\infty} \frac{1}{\mu n}\int_0^{\mu n} \sup_{r\in[-\mu,0]}\left(\frac{|||\theta_{r+q}\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}} dq \\ &= \quad \mathbb{E}\left(\sup_{r\in[-\mu,0]}\left(\frac{|||\theta_r\omega|||_{\beta',0,\mu} + \mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}}\right).\end{aligned}$$

Thanks to the ergodic theorem for continuous time (see [4]), we know that there exists a $\{\theta_t\}_{t\in\mathbb{R}}-$invariant set of full measure where this convergence is verified. In addition, we obtain that

$$\frac{1}{d} := \mu\mathbb{E}\left(\sup_{r\in[-\mu,0]}\left(\frac{|||\theta_r\omega|||_{\beta',0,\mu}+\mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}}\right) \geq \mu\mathbb{E}\left(\frac{\mu^{1-\beta'}}{\mu}\right)^{\frac{1}{\beta'}} = 1.$$

□

Now, we state two technical lemmas whose proofs can be found in [30]. Hence, we omit the corresponding proofs.

Lemma 4.3.3 *For any $\omega\in\Omega$ and $i\in\mathbb{N}$, let us denote $M_i(\omega)$ the random number of stopping times in the interval $(i\mu,(i+1)\mu]$. Then,*

$$M_i(\omega)\in\{N(\theta_{i\mu}\omega),N(\theta_{i\mu}\omega)+1\},$$

where $N(\cdot)$ was defined in Proposition 4.3.2.

Lemma 4.3.4 *Let $\mu\in(0,1)$. For any small $\delta>0$ such that $|||\omega|||_{\beta,0,\mu}<\delta$, there exists a $\{\theta_t\}_{t\in\mathbb{R}}-$invariant set of full measure Ω' and $\bar{d}=\bar{d}(\mu,\omega)$ such that, for $\omega\in\Omega'$,*

$$\limsup_{n\to+\infty}\frac{1}{n}\sum_{i=0}^{n-1}1_{M_j(\cdot)>N(\theta_{i\mu}\cdot)}(\omega)\leq\bar{d}.$$

Now, we establish the following result which will allow us to make some conclusions concerning the work made through the chapter.

Proposition 4.3.3 *Under the assumptions of Lemma 4.3.4, we have*

$$\liminf_{k\to+\infty}\frac{T_k(\omega)}{k}>D,$$

on a $\{\theta_t\}_{t\in\mathbb{R}}-$invariant set of full measure, where

$$D=D(\mu,\omega)=\frac{\mu d}{1+d\bar{d}}\in(0,\mu]$$

such that

$$\lim_{\mu\to0}D(\mu,\omega)=0,\qquad\lim_{\omega\to0}D(\mu,\omega)=\mu. \tag{4.31}$$

Proof. Let $M_j(\omega)\in\mathbb{N}$ be the random number of stopping times in $(j\mu,(j+1)\mu]$ for some $j\in\mathbb{Z}$. Then, given $k\in\mathbb{N}$, we can take $n=n(k,\omega)\in\mathbb{N}$ such that

$$\sum_{j=0}^{n-1}M_j(\omega)<k\leq\sum_{j=0}^{n}M_j(\omega).$$

Then, thanks to the order or the stopping times we know that

$$T_k(\omega) > T_{\sum_{j=0}^{n-1} M_j(\omega)}(\omega),$$

whence we obtain

$$\liminf_{k\to+\infty} \frac{T_k(\omega)}{k} \geq \liminf_{n\to+\infty} \frac{T_{\sum_{i=0}^{n-1} M_i(\omega)}(\omega)}{\sum_{i=0}^{n} M_i(\omega)} \geq \liminf_{n\to+\infty} \frac{(n-1)\mu}{\sum_{i=0}^{n} N(\theta_{i\mu}\omega) + \sum_{i=0}^{n} 1_{M_i(\cdot)>N(\theta_{i\mu}\cdot)}(\omega)},$$

where the last inequality can be deduced from the fact that $T_{\sum_{i=0}^{n-1} M_j(\omega)}(\omega)$ is the last stopping time in $((n-1)\mu, n\mu]$ and Lemma 4.3.3.

On the other hand, by taking into account (4.30) and Lemma 4.3.4, we have that

$$\begin{aligned}\limsup_{n\to+\infty} \frac{\sum_{j=0}^{n} N(\theta_{i\mu}\omega) + \sum_{j=0}^{n} 1_{M_j(\cdot)>N(\theta_{i\mu}\cdot)}(\omega)}{(n-1)\mu} &= \frac{1}{\mu} \limsup_{n\to+\infty} \frac{\sum_{j=0}^{n} N(\theta_{i\mu}\omega) + \sum_{j=0}^{n} 1_{M_j(\cdot)>N(\theta_{i\mu}\cdot)}(\omega)}{(n+1)\mu} \\ &\leq \frac{1}{\mu d} + \frac{1}{\mu}\bar{d},\end{aligned}$$

holds on a $\{\theta_t\}_{t\in\mathbb{R}}-$invariant set of full measure. Then, by defining

$$D = \frac{\mu d}{1 + d\bar{d}},$$

both properties in (4.31) are verified as long as the contribution of $|||\omega|||_{\beta,0,\mu}$ is small, since in this case, $d \to 1$ and $\bar{d} \to 0$.

□

We would like to remark that, thanks to Proposition 4.3.3, it is possible to consider a small noise such that condition (4.19) is Theorem 4.3.6 is clearly justified. Let us remember that condition (4.19) played an important role when obtaining the radius of the discrete absorbing set which allowed us to conclude the existence and uniqueness of the discrete random pullback attractor and, consequently, the existence and uniqueness of the continuous one. In addition, Proposition 4.3.3 also guarantees assumption (4.20) in Theorem 4.3.6 which, moreover, means that there are no accumulation points in the sequence of stopping times given by (4.14).

Remark 4.3.2 *We note that, as pointed out at the beginning of the chapter, the same analysis could be carried out for the corresponding stochastic chemostat model with wall growth affected by a fractional Brownian motion. To be more precise, we recall that it is also possible to rewrite the model with wall growth in the abstract formulation given by* (4.8) *such that Properties (P1)-(P3) are held in this case as well. In this way, we could redo the chapter again for the model with wall growth and the same results that the ones provided for the case without wall growth could be proved.*

4.3.4 Numerical simulations

In this section we will show some numerical simulations which allow us to see easily the effects caused by the fractional Brownian motion in the chemostat models for different values of the Hurst parameter. Even though only the model without taking into account the wall growth was analyzed, since the other one can be rewritten under the same abstract formulations and the same analysis could be made, we will state in this section some numerical simulations concerning both stochastic chemostat models. As in the previous chapters, the blue dashed lines represent the solution of the deterministic systems and the rest represent different realizations of the stochastic ones. In addition, a single panel with the phase plane is displayed in the case without wall growth whereas, when considering the case with wall growth, four different panels will be shown: there is a big one with the phase plane showing the general dynamics of our system and, apart from that, other three smaller ones are displayed in order to show the dynamics of the substrate and the different species individually. Moreover, the thick black asterisk denotes the initial value (s_0, x_{10}, x_{20}).

On the one hand, we show the following numerical simulations for the model without taking into account the wall growth. In Figure 4.1 we consider $s_{in} = 1$, $D = 1$, $a = 0.6$, $m = 3$ and we take $s_0 = 2.5$ and $x_0 = 5$ as initial pair. In addition, we consider $\alpha = 0.1$ as intensity of the noise and the Hurst parameter is given by $H = 0.7$ (left) and $H = 0.9$ (right). It is not difficult to observe that we obtain persistence.

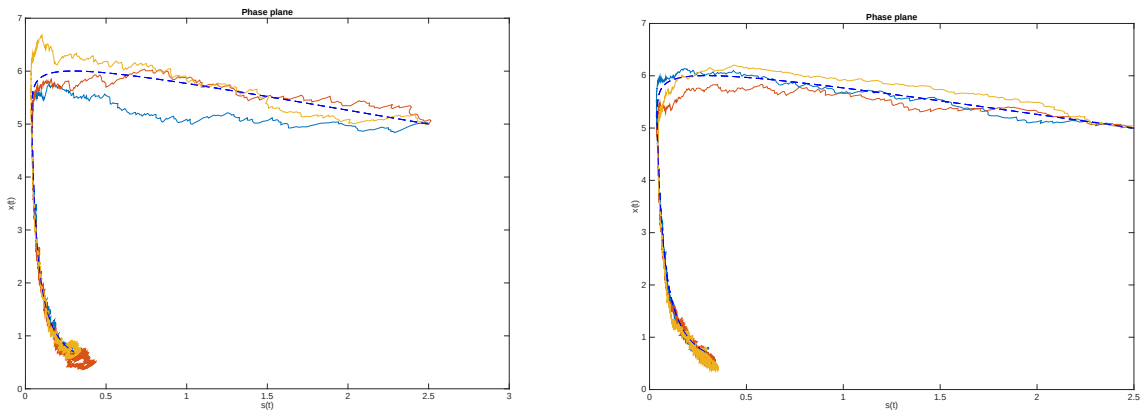


Figure 4.1: Persistence. $H = 0.7$ (left) and $H = 0.9$ (right)

Henceforth, we only mention those parameters which change respect to the ones used in the previous figure. In Figure 4.2 we increase the dilution rate to $D = 2$ and decrease $m = 1.5$. In this case, we consider $H = 0.7$ (left) and $H = 0.9$ (right) as the Hurst parameters. As a result, we can observe that the realizations obtained in the case of $H = 0.9$ seem to be more regular, which is not surprising due to the fact that the higher the Hurst parameter is, then the more regular the fractional Brownian motion is.

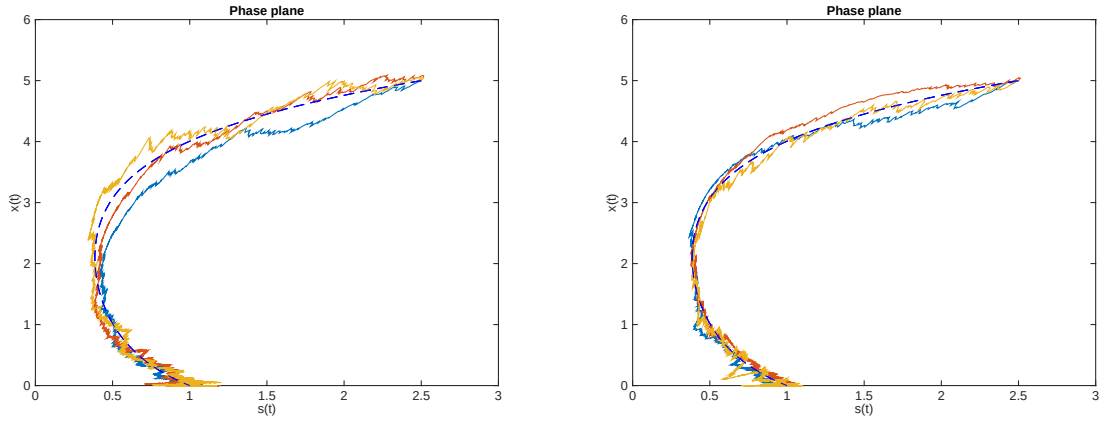


Figure 4.2: Extinction. $H = 0.7$ (left) and $H = 0.9$ (right)

On the other hand, regarding the stochastic chemostat model with wall growth, in Figure 4.3 we consider $s_{in} = 1$, $D = 2$, $a = 0.6$, $m = 5$, $b = 0.5$, $\nu = 2$, $c = 1.2$, $r_1 = 0.2$, $r_2 = 0.8$ and we take $s_0 = 5$, $x_{10} = 10$ and $x_{20} = 10$ as initial triple. In addition, we consider $\alpha = 0.1$ as intensity of the noise and the Hurst parameter is given by $H = 0.7$. Therefore, we obtain the extinction of both microorganisms.

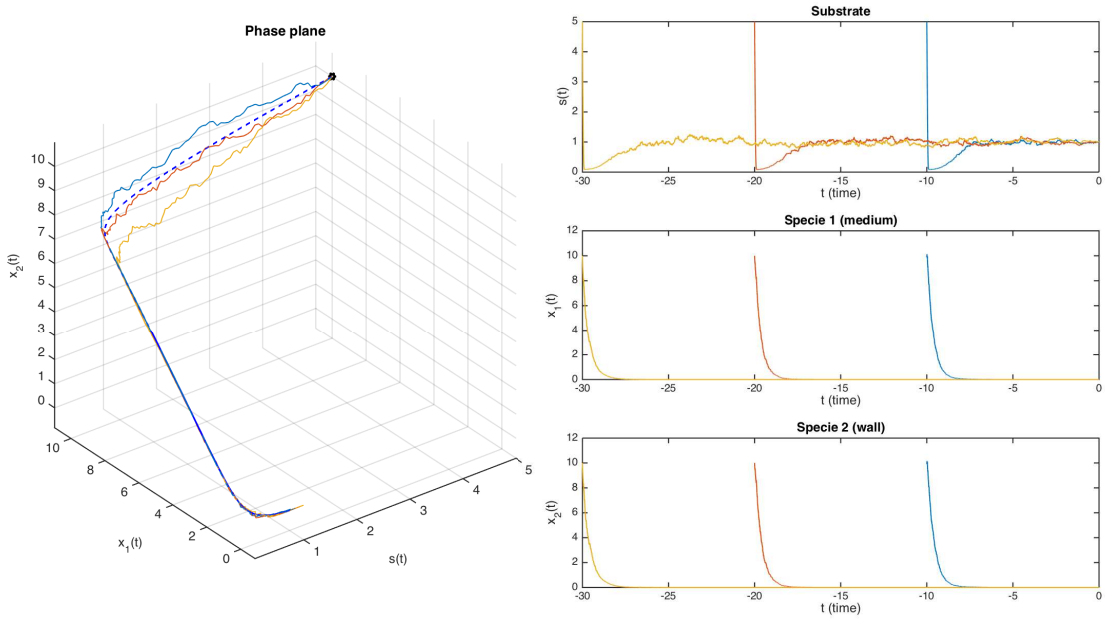


Figure 4.3: Extinction. $H = 0.7$

In Figure 4.4 we increase the Hurst parameter to $H = 0.9$. Therefore, we can also observe in this figure that the realizations of the solutions of the corresponding model seem to be more regular when comparing them with the ones obtained in Figure 4.3. As pointed out before, it is quite logical by taking into account the properties concerning the fractional Brownian motion which were introduced at the beginning of the chapter.

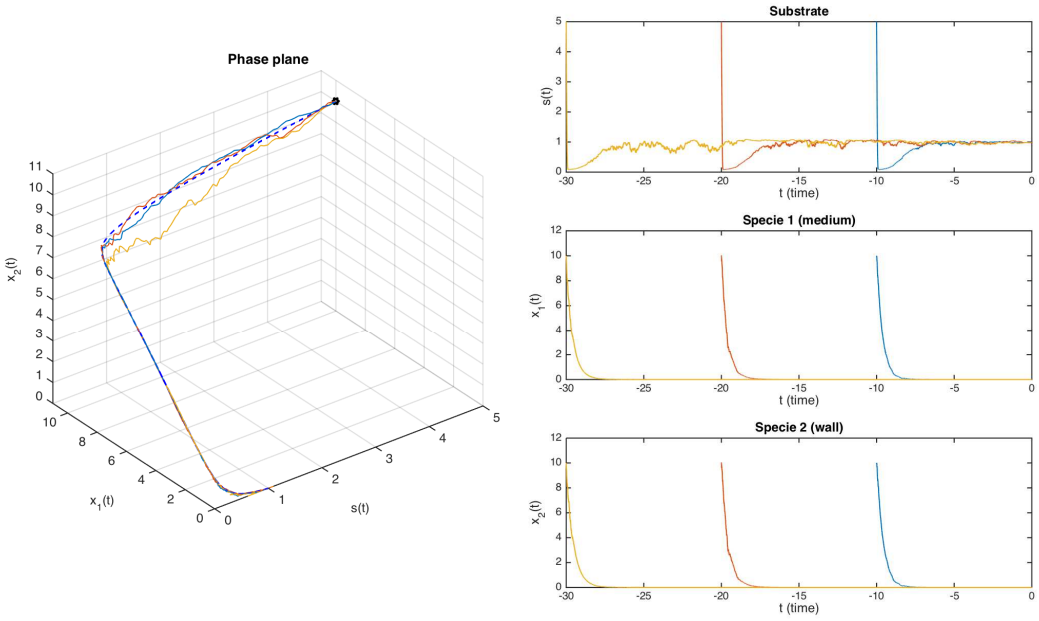


Figure 4.4: Extinction. $H = 0.9$

In Figure 4.5 we consider again $H = 0.7$ as the Hurst parameter. In this case, we decrease the collective death rate to $\nu = 0.3$ and increase the growth rate of the species to $c = 3$. Therefore, by taking into account that ν represents the collective death rate of the species and c denotes the corresponding consumption rate, it is logical that we obtain persistence.

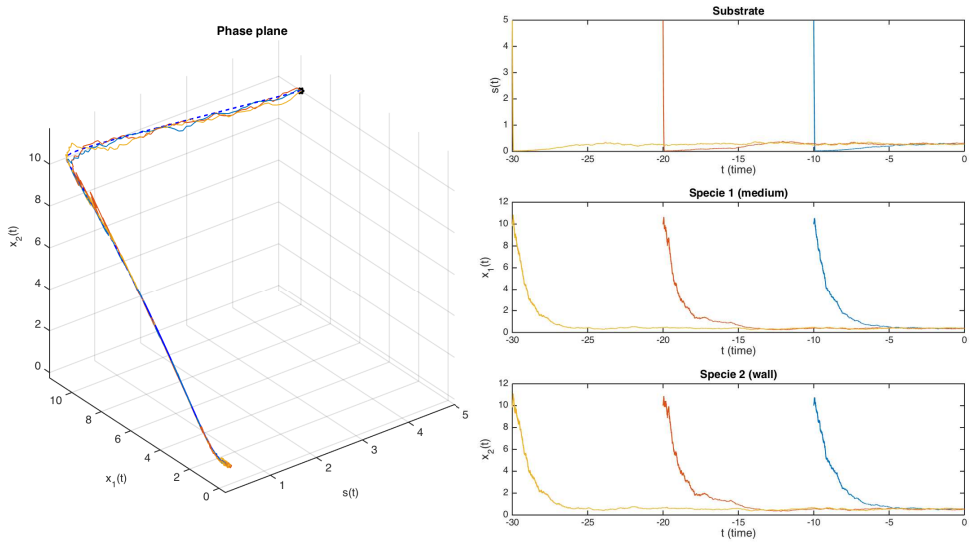


Figure 4.5: Extinction. $\alpha = 0.1$

Eventually, in Figure 4.6 we increase the Hurst parameter to $H = 0.9$ and, then, we can also observe that we have persistence.

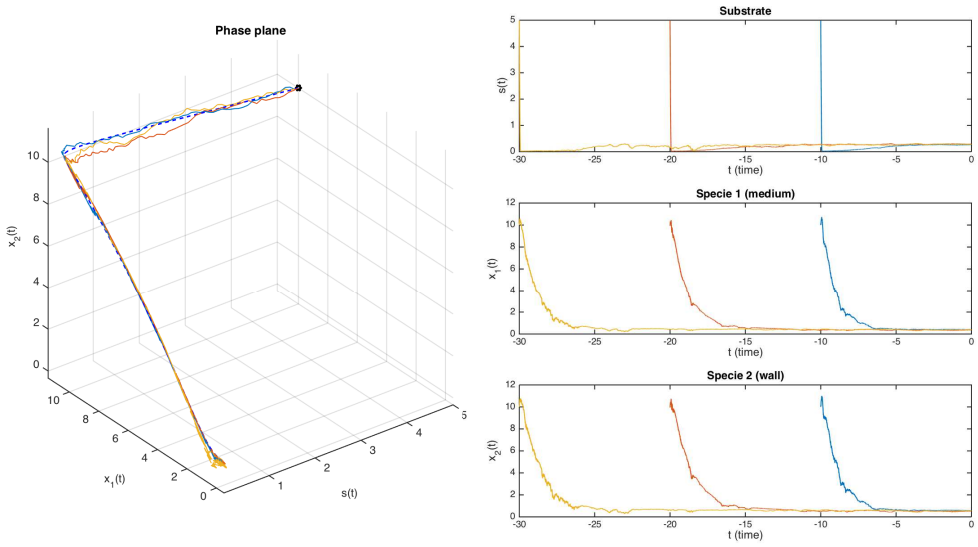


Figure 4.6: Extinction. $\alpha = 0.1$

Finally, we would like to note that it does not seem to be an important difference when comparing the numerical simulations shown in this chapter with the ones in Chapter 3, specially when the Hurst parameter is closed to $H = 0.5$ which is quite logical since, as we know, the fBm is the standard one when $H = 0.5$.

Appendix

APPENDIX A

Preliminaries on stochastic processes

In this chapter we will introduce some basic preliminaries on stochastic process, paying special attention to the well-known standard Wiener process and also to the Ornstein-Uhlenbeck process, which are the ones used in this dissertation, apart from the fractional Brownian motion which is presented in Chapter 4 for convenience in order to make our presentation as much clear as possible.

Definition A.0.1 *Let be $(\Omega, \mathscr{F}, \mathbb{P})$ a probability space. Then, a standard Wiener process is a family of random variables $W(t)(\cdot) : \omega \in \Omega \to W(t)(\omega) \in \mathbb{R}$, where $t > 0$, such that the following properties are fulfilled $\mathbb{P}-$almost surely:*

- *It holds $W(0) = 0$.*
- *The mapping*

$$t \in \mathbb{R}^+ \to W(\omega) \in \mathbb{R}$$

  has continuous, but not bounded variation, paths.

- *It has independent increments, i.e., for $0 < t_1 < \cdots < t_n$, the random variables*

$$W(t_1),\ W(t_2) - W(t_1),\ \ldots,\ W(t_n) - W(t_{n-1})$$

  are independent.

- *It is stationary, i.e., the joint distribution of*

$$\{W(t_1 + t), \ldots, W(t_k + t)\}$$

does not depend on t.

- *The random variable $W(t) - W(s)$, $0 \le s \le t$, is Gaussian with mean zero and variance $t - s$.*

Let W be a two sided Wiener process. Kolmogorov's theorem ensures that W has a continuous version, that we will denote by ω, whose canonical interpretation is as follows: let Ω be defined by

$$\Omega = \{\omega \in \mathscr{C}(\mathbb{R}, \mathbb{R}) : \omega(0) = 0\} = \mathscr{C}_0(\mathbb{R}, \mathbb{R}),$$

$\mathscr{F}$ be the Borel $\sigma-$algebra on Ω generated by the compact open topology (see [4] for details) and $\mathbb{P}$ the corresponding Wiener measure on $\mathscr{F}$. We consider the Wiener shift flow given by

$$\theta_t\omega(\cdot) = \omega(\cdot + t) - \omega(t), \quad t \in \mathbb{R},$$

then $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$ is a metric dynamical system.

Now let us introduce the following Ornstein-Uhlenbeck process on $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$

$$z^*(\theta_t\omega) = -\int_{-\infty}^{0} e^s \theta_t\omega(s)\,ds, \quad t \in \mathbb{R}, \quad \omega \in \Omega, \tag{A.1}$$

which solves the following Langevin equation (see [4, 19])

$$dz + z\,dt = d\omega(t), \quad t \in \mathbb{R}. \tag{A.2}$$

Proposition A.0.1 *(see [4, 19]) There exists a θ_t-invariant set $\widetilde{\Omega} \in \mathscr{F}$ of Ω of full $\mathbb{P}$ measure such that for $\omega \in \widetilde{\Omega}$, we have*

(i) the random variable $|z^*(\omega)|$ is tempered.

(ii) the mapping

$$(t, \omega) \to z^*(\theta_t\omega) = -\int_{-\infty}^{0} e^s \omega(t+s)\mathrm{d}s + \omega(t)$$

is a stationary solution of (A.2) *with continuous trajectories;*

(iii) in addition, for any $\omega \in \tilde{\Omega}$:

$$\begin{aligned}
\lim_{t\to\pm\infty} \frac{|z^*(\theta_t\omega)|}{t} &= 0;\\
\lim_{t\to\pm\infty} \frac{1}{t}\int_0^t z^*(\theta_s\omega)\,ds &= 0;\\
\lim_{t\to\pm\infty} \frac{1}{t}\int_0^t |z^*(\theta_s\omega)|\,ds &= \mathbb{E}[z^*] < \infty.
\end{aligned}$$

In what follows we will consider the restriction of the Wiener shift θ to the set $\tilde{\Omega}$, and we restrict accordingly the metric dynamical system to this set, that is also a metric dynamical system, see [14]. For simplicity, we will still denote the restricted metric dynamical system by the old symbols $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$.

APPENDIX B

Preliminaries on random dynamical systems

In this section we present some basic preliminaries related to random dynamical systems and random attractors which are necessary for our analysis along the whole dissertation. For more detailed information about random dynamical systems and their importance, we refer the readers to [4].

Let $(\mathscr{X}, \|\cdot\|_{\mathscr{X}})$ be a separable Banach space and let $(\Omega, \mathscr{F}, \mathbb{P})$ be a probability space where $\mathscr{F}$ is the $\sigma-$algebra of measurable subsets of Ω (called "events") and $\mathbb{P}$ is the probability measure. To connect the state ω in the probability space Ω at time 0 with its state after a time of t elapses, we define a flow $\theta = \{\theta_t\}_{t\in\mathbb{R}}$ on Ω with each θ_t being a mapping $\theta_t : \Omega \to \Omega$ that satisfies

(1) $\theta_0 = \mathrm{Id}_\Omega$,

(2) $\theta_s \circ \theta_t = \theta_{s+t}$ for all $s, t \in \mathbb{R}$,

(3) the mapping $(t, \omega) \mapsto \theta_t\omega$ is measurable,

(4) the probability measure $\mathbb{P}$ is preserved by θ_t, i.e., $\theta_t\mathbb{P} = \mathbb{P}$.

This set-up establishes a time-dependent family θ that tracks the noise, and $(\Omega, \mathscr{F}, \mathbb{P}, \theta)$ is called a *metric dynamical system* (see [4]).

Definition B.0.1 *A stochastic process $\{\varphi(t,\omega)\}_{t\geq 0,\omega\in\Omega}$ is said to be a continuous RDS over $(\Omega, \mathscr{F}, \mathbb{P}, \{\theta_t\}_{t\in\mathbb{R}})$ with state space $\mathscr{X}$ if $\varphi : [0,+\infty) \times \Omega \times \mathscr{X} \to \mathscr{X}$ is $(\mathscr{B}[0,+\infty) \times \mathscr{F} \times \mathscr{B}(\mathscr{X}), \mathscr{B}(\mathscr{X}))$- measurable, and for each $\omega \in \Omega$,*

(i) the mapping $\varphi(t,\omega) : \mathscr{X} \to \mathscr{X}$, $x \mapsto \varphi(t,\omega)x$ is continuous for every $t \geq 0$,

(ii) $\varphi(0,\omega)$ is the identity operator on $\mathscr{X}$,

(iii) *(cocycle property)* $\varphi(t+s,\omega)=\varphi(t,\theta_s\omega)\varphi(s,\omega)$ *for all* $s,t\geq 0$.

Definition B.0.2 *Let* $(\Omega,\mathscr{F},\mathbb{P})$ *be a probability space. A random set* K *is a measurable subset of* $\mathscr{X}\times\Omega$ *with respect to the product* $\sigma-$*algebra* $\mathscr{B}(\mathscr{X})\times\mathscr{F}$.

The $\omega-$*section of a random set* K *is defined by*

$$K(\omega)=\{x:(x,\omega)\in K\},\quad \omega\in\Omega.$$

In the case that a set $K\subset\mathscr{X}\times\Omega$ *has closed or compact* $\omega-$*sections it is a random set as soon as the mapping* $\omega\mapsto d(x,K(\omega))$ *is measurable (from* Ω *to* $[0,\infty)$*) for every* $x\in\mathscr{X}$*, see [27]. Then* K *will be said to be a closed or a compact, respectively, random set. It will be assumed that closed random sets satisfy* $K(\omega)\neq\emptyset$ *for all or at least for* $\mathbb{P}-$*almost all* $\omega\in\Omega$.

Remark B.0.1 *We note that in the literature very often random sets are defined provided that* $\omega\mapsto d(x,K(\omega))$ *is measurable for every* $x\in\mathscr{X}$*. Obviously this is satisfied, for instance, when* $K(\omega)=N$ *for all* ω*, where* N *is some non-measurable subset of* $\mathscr{X}$*, and also when* $K=(U\times F)\cup(\overline{U}\times F^c)$ *for some open set* $U\subset\mathscr{X}$ *and* $F\notin\mathscr{F}$*. In both cases* $\omega\mapsto d(x,K(\omega))$ *is constant, hence measurable, for every* $x\in\mathscr{X}$*. However, both cases give* $K\subset\mathscr{X}\times\Omega$ *which is not an element of the product* $\sigma-$*algebra* $\mathscr{B}(\mathscr{X})\times\mathscr{F}$.

Definition B.0.3 *A bounded random set* $K(\omega)\subset\mathscr{X}$ *is said to be* tempered with respect to $\{\theta_t\}_{t\in\mathbb{R}}$ *if for a.e.* $\omega\in\Omega$*,*

$$\lim_{t\to\infty}e^{-\beta t}\sup_{x\in K(\theta_{-t}\omega)}\|x\|_{\mathscr{X}}=0,\quad \text{for all } \beta>0;$$

a random variable $\omega\mapsto r(\omega)\in\mathbb{R}$ *is said to be* tempered with respect to $\{\theta_t\}_{t\in\mathbb{R}}$ *if for a.e.* $\omega\in\Omega$*,*

$$\lim_{t\to\infty}e^{-\beta t}\sup_{t\in\mathbb{R}}|r(\theta_{-t}\omega)|=0,\quad \text{for all } \beta>0.$$

In what follows we use $\mathscr{E}(\mathscr{X})$ to denote the set of all tempered random sets of $\mathscr{X}$.

Definition B.0.4 *A random set* $B(\omega)\subset\mathscr{X}$ *is called a* random absorbing set *in* $\mathscr{E}(\mathscr{X})$ *if for any* $E\in\mathscr{E}(\mathscr{X})$ *and a.e.* $\omega\in\Omega$*, there exists* $T_E(\omega)>0$ *such that*

$$\varphi(t,\theta_{-t}\omega)E(\theta_{-t}\omega)\subset B(\omega),\quad \forall\, t\geq T_E(\omega).$$

Definition B.0.5 *Let* $\{\varphi(t,\omega)\}_{t\geq0,\omega\in\Omega}$ *be an RDS over* $(\Omega,\mathscr{F},\mathbb{P},\{\theta_t\}_{t\in\mathbb{R}})$ *with state space* $\mathscr{X}$ *and let* $A(\omega)(\subset\mathscr{X})$ *be a random set. Then* $\mathscr{A}=\{A(\omega)\}_{\omega\in\Omega}$ *is called a* global random $\mathscr{E}-$attractor (or pullback $\mathscr{E}-$attractor) for $\{\varphi(t,\omega)\}_{t\geq0,\omega\in\Omega}$ *if*

(i) *(compactness)* $A(\omega)$ *is a compact set of* $\mathscr{X}$ *for any* $\omega\in\Omega$*;*

(ii) *(invariance) for any* $\omega\in\Omega$ *and all* $t\geq0$*, it holds*

$$\varphi(t,\omega)A(\omega)=A(\theta_t\omega);$$

(iii) *(attracting property) for any $E \in \mathscr{E}(\mathscr{X})$ and a.e. $\omega \in \Omega$,*

$$\lim_{t\to\infty} \operatorname{dist}_{\mathscr{X}}(\varphi(t,\theta_{-t}\omega)E(\theta_{-t}\omega), A(\omega)) = 0,$$

where

$$\operatorname{dist}_{\mathscr{X}}(G,H) = \sup_{g\in G}\inf_{h\in H}\|g-h\|_{\mathscr{X}}$$

is the Hausdorff semi-metric for $G, H \subseteq \mathscr{X}$.

Proposition B.0.1 *(See [20, 33]) Let $B \in \mathscr{E}(\mathscr{X})$ be a closed absorbing set for the continuous random dynamical system $\{\varphi(t,\omega)\}_{t\geq 0,\omega\in\Omega}$ that satisfies the asymptotic compactness condition for $a.e.\ \omega \in \Omega$, i.e., each sequence $x_n \in \varphi(t_n, \theta_{-t_n}\omega)B(\theta_{-t_n}\omega)$ has a convergent subsequence in $\mathscr{X}$ when $t_n \to \infty$. Then φ has a unique global random attractor $\mathscr{A} = \{A(\omega)\}_{\omega\in\Omega}$ with component subsets*

$$A(\omega) = \bigcap_{\tau\geq T_B(\omega)} \overline{\bigcup_{t\geq\tau} \varphi(t,\theta_{-t}\omega)B(\theta_{-t}\omega)}.$$

If the pullback absorbing set is positively invariant, i.e., $\varphi(t,\omega)B(\omega) \subset B(\theta_t\omega)$ for all $t \geq 0$, then

$$A(\omega) = \bigcap_{t\geq 0} \overline{\varphi(t,\theta_{-t}\omega)B(\theta_{-t}\omega)}.$$

Remark B.0.2 *When the state space $\mathscr{X} = \mathbb{R}^d$ as in this paper, the asymptotic compactness follows trivially. Note that the random attractor is path-wise attracting in the pullback sense, but does not need to be path-wise attracting in the forward sense, although it is forward attracting in probability, due to some possible large deviations, see e.g. [4].*

The next result ensures when two random dynamical systems are conjugated (see also [14, 15, 18]).

Lemma B.0.1 *(See [14]) Let φ_u be a random dynamical system on $\mathscr{X}$. Suppose that the mapping $\mathscr{T} : \Omega\times\mathscr{X} \to \mathscr{X}$ possesses the following properties: for fixed $\omega \in \Omega$, $\mathscr{T}(\omega,\cdot)$ is a homeomorphism on $\mathscr{X}$, and for $x \in \mathscr{X}$, the mappings $\mathscr{T}(\cdot,x)$, $\mathscr{T}^{-1}(\cdot,x)$ are measurable. Then the mapping*

$$(t,\omega,x) \to \varphi_v(t,\omega)x := \mathscr{T}^{-1}(\theta_t\omega, \varphi_u(t,\omega)\mathscr{T}(\omega,x))$$

is a (conjugated) random dynamical system.

Eventually, the next result stablished the connection between both attractors when applying the conjugation Lemma B.0.1.

Lemma B.0.2 *There is a one-to-one corresponding between the attractors of φ_u and φ_v. In particular, if $\mathscr{A}(\omega)$ is a random pullback attractor of φ_u, then $\mathscr{A}^{\mathscr{T}}(\omega) := \mathscr{T}^{-1}(\omega)\mathscr{A}(\omega)$ is a random pullback attractor of φ_v. Conversely, if $\mathscr{A}^{\mathscr{T}}(\omega)$ is a random pullback attractor of φ_v, then $\mathscr{A}(\omega) := \mathscr{T}(\omega)\mathscr{A}^{\mathscr{T}}(\omega)$ is a random pullback attractor of φ_u.*

APPENDIX C

A new discrete Gronwall Lemma

In this section, we prove some technical results which will lead into a discrete Gronwall Lemma.

Lemma C.0.1 *The following formula is true*

$$1+\sum_{k=q}^{n-1} g_k \prod_{j=k+1}^{n-1}(1+g_j)=\prod_{j=q}^{n-1}(1+g_j).$$

Proof. It is straightforward to check that

$$\begin{aligned}
&1+\sum_{k=q}^{n-1} g_k \prod_{j=k+1}^{n-1}(1+g_j)\\
=\;& 1+g_{n-1}+g_{n-2}(1+g_{n-1})+g_{n-3}(1+g_{n-1})(1+g_{n-2})+\cdots+g_q(1+g_{n-1})(1+g_{n-2})\cdots(1+g_{q+1})\\
=\;& (1+g_{n-1})(1+g_{n-2}+g_{n-3}(1+g_{n-2})+\cdots+g_q(1+g_{n-2})(1+g_{n-3})\cdots(1+g_{q+1}))\\
=\;& (1+g_{n-1})(1+g_{n-2})(1+g_{n-3}+\cdots+g_q(1+g_{n-3})\cdots(1+g_{q+1}))\\
=\;& \prod_{j=q}^{n-1}(1+g_j),
\end{aligned}$$

is fulfilled, by repeating the process till the last factor. □

Lemma C.0.2 *Let $\{g_n\}_{n\geq 0}$ be a sequence. For $n \geq 0$ we define*

$$G_n := \prod_{j=0}^{n-1} (1 + g_j) \tag{C.1}$$

Then, for $n \geq 0$ and $0 \leq k \leq n$, we have

$$G_n = 1 + \sum_{j=0}^{n-1} g_j G_j \qquad \text{and} \qquad G_n = G_k + \sum_{j=k}^{n-1} g_j G_j. \tag{C.2}$$

Proof. The result follows easily by induction, so the proof is omitted.

□

Lemma C.0.3 *Assume $\{y_n\}_{n\geq 0}$, $\{f_n\}_{n\geq 0}$ and $\{g_n\}_{n\geq 0}$ are non-negative sequences such that*

$$y_n \leq f_n + \sum_{k=0}^{n-1} g_k y_k \tag{C.3}$$

is fulfilled. Then, for $n \geq 0$, we have

$$y_n \leq f_n + \sum_{0\leq k<n} f_k g_k \prod_{k<j<n} (1 + g_j). \tag{C.4}$$

Proof. We will prove this result by using an induction argument. From (C.3) we know that $y_0 \leq f_0$, then (C.4) follows directly for $n = 0$. Suppose now that (C.4) holds true for $0 \leq n < m$ whence we have

$$\begin{aligned}
y_m &\leq f_m + \sum_{k=0}^{m-1} g_k y_k \\
&\leq f_m + \sum_{k=0}^{m-1} \left\{ f_k + \sum_{l=0}^{k-1} f_l g_l \prod_{j=l+1}^{k-1} (1 + g_j) \right\} g_k \\
&= f_m + g_{m-1} f_{m-1} + \sum_{k=0}^{m-2} g_k f_k + \sum_{k=0}^{m-2} \sum_{l=k+1}^{m-1} g_l f_k g_k \frac{G_l}{G_{k+1}} \\
&= f_m + g_{m-1} f_{m-1} + \sum_{k=0}^{m-2} f_k g_k \frac{1}{G_{k+1}} \left\{ G_{k+1} + \sum_{l=k+1}^{m-1} g_l G_l \right\} \\
&= f_m + \sum_{k=0}^{m-1} f_k g_k \prod_{j=k+1}^{m-1} (1 + g_j).
\end{aligned}$$

□

Now, let us define, for $k \in \mathbb{N}^+$, the following sum

$$f_k := \sum_{q=0}^{k} \psi_q. \tag{C.5}$$

Thanks to the previous technical results, we can prove the following Discrete Gronwall Lemma.

Lemma C.0.4 (Discrete Gronwall Lemma) *Assume that $\{y_n\}_{n\geq 0}$, $\{f_n\}_{n\geq 0}$ and $\{g_n\}_{n\geq 0}$ are non-negative sequences. Then, provided*

$$y_n \leq f_n + \sum_{k=0}^{n-1} g_k y_k, \tag{C.6}$$

we have

$$y_n \leq \psi_0 \prod_{j=1}^{n-1}(1+g_j) + \sum_{q=1}^{n} \psi_q \prod_{j=q+1}^{n-1}(1+g_j).$$

Proof. Thanks to Lemma C.0.1, Lemma C.0.3 and taking into account the definition (C.5), from (C.6) we can deduce the following calculations

$$\begin{aligned}
y_n &\leq f_n + \sum_{k=0}^{n-1} f_k g_k \prod_{j=k+1}^{n-1}(1+g_j) \\
&= \sum_{q=0}^{n} \psi_q + \sum_{k=0}^{n-1}\left(\sum_{q=0}^{k}\psi_q\right) g_k \prod_{j=k+1}^{n-1}(1+g_j) \\
&= \psi_n + \sum_{q=0}^{n-1} \psi_q \left(1 + \sum_{k=q}^{n-1} g_k \prod_{j=k+1}^{n-1}(1+g_j)\right) \\
&= \psi_n + \sum_{q=0}^{n-1} \psi_q \prod_{j=q}^{n-1}(1+g_j) \\
&= \psi_0 \prod_{j=0}^{n-1}(1+g_j) + \sum_{q=1}^{n}\prod_{j=q}^{n-1}(1+g_j),
\end{aligned}$$

whence we can conclude the proof. □

List of Figures

List of Tables

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